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ACL20245 Rattus no
ACC97362 Rattus no
CQ842051 Sequence
AKL23581 Homo sapi
ACC17081 Homo sapi
ACC17081 Sequence
G76816 S208P6606FG
AX00443 Sequence
BV053534 S212P6219
CQ736905 Sequence
CQ74096 Sequence
CQ741025 Drosophil
AKT32376 Drosophil
AKT32377 Ciona int
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BC059819 Mus muscu
BX005084 Mouse DNA
                                                       .; Search time 16939.5 Seconds (without alignments) 11655.272 Million cell updates/sec
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                                                                                                                  Description
                                                                                                                                                                                       9053458
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                    4526729 seqs, 23644849745 residues
                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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CQ736905
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                                       nucleic search, using sw model
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AL158206 Human DNA			AF347024 Homo sapi	m.	CQ605547 Sequence	AK024898 Homo sapi	AL391834 Human DNA						CQ492742 Sequence		CQ605546 Sequence	AC017332 Drosophil	_			AC093044 Drosophil	CQ731034 Sequence			n	AL670603 Mouse DNA
AL158206	AC109451	AX206797	AF347024	AF347023	CO605547	AK024898	AL391834	AC109451	AR419744	AX980438	BD115297	CQ492597	CQ492742	CQ493050	CQ605546	AC017332	AC004364	AE003665	AC009252	AC093044	CQ731034	CQ615131	AC017406	AC108371	AL670603
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183.6	183.6	174.8	174.8	173.8	160.6	131.2	124	124	114.2	114.2	114.2	108	108	108	92.6	92.6	92.6	92.6	92.6	92.6	78.4	77.8	77.8	75.4	72
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ALIGNMENTS

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AF282864 4174 bp mRNA linear ROD 12-DEC-2001
Mus musculus cancer related gene-liver 1 mRNA, complete cds.
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Lases 1 to 4174)
Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J. Expression profiling and identification of novel genes in hepatocellular carcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dases 1 to 4174)
Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Garation of genes deregulated in murine hepatocellular
carcinomes using oligonucleotide microarrays and representational
difference analysis
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Submitted (27-UN-2000) Oncology, University of Wisconsin, 1400
University Avenue, Madison, WI 53706, USA
Location/Qualifiers
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Farnham, P.J. and Graveel, C.R.
                                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
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961 TGGTGTGGGTGTTTAAAATTCTGGTCCTTTGTGATCTAACTGGACCACTGTGCCTGACCT 1020 	1021 CCCTAGGITAAGIAGGGCTCAGGACATAAGGIGTCTTCCTCAGTATCCTTTCCAGGC 1080	1081 ATACGGGCTTGCTGGGGTTATGTCCATAATGACATCAACAGAGTAGTTCTTTGGGAGACCT 1140 	1141 AGGCAACCCAAAGTTCTTGCTGGAGGGGGGGGGGTGCTGTTCCACCATTTCCAGACT 1200 	1201 CTCAACCCCTGATAAACAAGACCTTCTGATTTGGTGATGAAAGGTTCCAGAACTTTTCA 1260 	1261 TTTTGCCGGGAGAAACTGTCCTTCAACAAAACCAAGTGGGCAAAACGAAACGCTGTGGGGGGTG 1320 	1321 TGACTAAGACGGGGGTTGTCACTCGCACCTCTTAGCTTTCCCAGGTTCTCCACGTGTT 1380	1381 TGTGGATCCTTCCACTACCTGTGAGAGATGGAGCCACGGCTTCAGAGGGCAAAGCTG 1440 	1441 GCAACACTCTATGCCAAAAGCTACACTCCTTTTAAGCACACTTTACATAGACACTAT 1500 	1501 TICTGCTCTTCCAGAGTGCAGCAGCCTCAGACCCACAGAGAATCCTTCAGGTTATGTGAA 1560 	1561 GATTCCACACACCCCTCTTGTGACCTCTGTGACAGCCACGTTGTAATCGCG 1620 	1621 GAGGCAGCTCTGGAGGCTTGACTGTGGAGCGCCTGTGAAGATTTTGGAAAGCTTTTCTTA 1680 	1681 TIGGAAGCTITIGGIGITGITGITACCICCAAGAITCIGACCCCGITICICIGGTGITITI 1740 	1741 AGGGGATAIGIGCTICCIGAGIGACGTAGCCTCCCTAGGAIGIGGGCCTCCGGCTTIGT 1800 	1801 TITCATAATACCIGGIGCTAACIGGITICICAGAGCACTITGCICTICITGIAGGCTGGGC 1860 	1861 GGTCACTACACTCTGATTGGCTGGGGATCCCAGGGAGGAGGAGGACACACTCTGACA 1920 	1921 IGAAIGICICCICCCIGCAICCIACTGICTICACIGGCICICTICAGGGIAIGAAGIGG 1980 	1981 GTATGGGGTATCTCAGGGATGTTTGTAACTCAGGCACCTTCTGCTTTCTGACATTCCATT 2040
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LPPICMCLFRQYATCFNSGIYLIWTLLVVVGIGSVYFHATLSFLGQMLDELAILWVLM CALAMWFPRRYLPKIFRNDRGRFRAVVCVLSAITTCLAFIKPAINNISLAILGLPCTA LLVAELKRCDNVRVFKLGLFSGLWWTLALFCRISDQAFCELLSSFHFPYLHCVHHILI CLASYLGCVCFAYFDAASEIPBQGPVIRFWPSEKWAFIGVPYVGLLCAHKKSPVKIT"	Query Match 100.0%; Score 4174; DB 10; Length 4174; Best Local Similarity 100.0%; Pred. No. 0; Matches 4174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 GGCACGAGGGCTCCGATGCTCCAGAGCGGCCATGGGCGCCCCGGCATGGGACCA 60 Db 1 GGCACGAGGGTTGCTCCGAAGCGGCCATGGGCGCCCCGCATGGTGGAACCA 60	Qy 61 CCTGCGGGCTGGCAGTTCGGAGGTGCGAGGACAACTACGTACTATCGTGCCTGC 120 Db 61 CCTGCGGGCTGGCATTCGGAGGTGGATTGGTGCGAGGACAACTACACTATCGTGCTGC 120	10.10 10.10 10.10	0 0	QY 241 GCTCCTAGTIGIAGIGGGATIGGATCTGTCTACTTCCATGCAACGCTGAGTTTCCTGGG 3.00 Db 241 GCTCCTAGTIGIAGIGGGATTGGATCTGTCTACTACCATGCAACGCTGAGTTTCCTGGG 3.00		OY 361 TCCCAGGAGGTATTTACCAAAGATCTTTCGGAATGACAGGGCAGGTTCAAGGCAGTGGT 420 Db 361 TCCCAGGAGGTATTTACCAAAGATCTTTCGGAATGACAGGGCAGGTTCAAGGCAGTGGT 420	OY 421 GTGTGTCCTGTCTGCAATTACAACGTGCTTGGCGTTTATCAAGCCCGCCATCAACAATAT 480 Db 421 GTGTGTCTGTCTGCAATTACAACGTGCTTGGCGTTTATCAAGCCCGCCATCAACAATAT 480	Ay 481 TICCTGAIGATTTCTGGGACTTCCATGCGCTGCTTGTTGCAGAGCTGAAGGGTG 540		CTA	OY 661 CCTGCACTGTGTGCATATTCTCATCTGCTTGCTTCGTACCTGGGCTGTGTGCTT 720	ပ္ဘ <u>—</u> ပ္ပ	Oy 781 CAGCGAGAAATGGGCTTTTATTGGTGTCCCTTATGTGTCCCTTCTGTGGCCCACAAGAA 840 Db 781 CAGCGAGAAATGGGCTTTTATTGGTGTCCCTTATGTGTCCCTTCTGTGTGCCCACAAGAA 840	OY 841 GTCGCCAGTCAAGATCACGTGATGGCAAGGCAGTGACCAGCTTCTCTACTTCTATT 900 Db 841 GTCGCCAGTCAAGATCACGTGATGGCAAGGCAGTGACCAGCTTCTCTACTTCTATT 900	Oy 901 CGAGTGCGCGCTGGGCTTCGTTTGCTAGGAAAGATGGCTGAGGGGTTGAGGAATTGGTG 960

CTGGGACCAGGGGACACTCCAAGGGAAGCCCGGTAACCGATGGACCACTGGGCCCTGCAGATC TTCTCCCTTCTGGTAGAGATGACATCGATGAGTGATGTCGTGACCACTGGGCCCTGCAGATC TTCTCCCTTCTGTAGAGATGACATCGATGAGTGATGTCGTGACCACTGGGCCCTGCAGA TTCTCCCTTCTGTAGAGATGACATCGATGAGTGATCTCAGGACCACTGGGCCCTGCAGA GGGGGCTCTGTTCTGT	4021 AGHATHTAACCATAGCTCTGGGAGGATTTACAGACCTTTTGCACTTTATGCTTTTTTG 4080 4081 TGAACTCTGATAACCATGGTCAATATTAAAGCCAATAACCGGCATTTTCTGTGAATAAAC 4140 4081 TGAACTCTGATAACCATGGTCAATATTAAAGCCAATAACTGGCATTTTCTGTGAATAAAC 4140 4141 ATGCATATGTATCTAAAAAAAAAAAAAAAAAA 4174 4141 ATGCATATGTATCTAAAAAAAAAAAAAAAAAAA 4174 4141 ATGCATATGTATCTAAAAAAAAAAAAAAAAAAAAAA 4174
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CTTCTGGGTGAGACTCCACGGGGACTGGAGTTGGAACACCGTTCTGGGTGGG	

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LPPICMCLFRQYATCFNSGIYLIWTLLVVVGIGSVYFHATLSFLGQMLDELAILWVLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGCTCCGATGCTCCAGAGCGCCATGGGCCCCCGCACTGGTGGGACCACCTGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGATGAACTTGCCATTCTGTGGGTTCTGATGTGTGCTTTTGGCCATGTGGGTTTCCCAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.6%; Score 3864.4; 96.6%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                   codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAHKKSPVKIT
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Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Altschul, S.E., Zeeberg, B., Buetc, Schemen, C.M., Schuler, G.D.,
Altschul, S.E., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, N.K.,
Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, R.F.,
Stapleron, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boask, S.A., McBwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Villalon, D.K., Malek, J.A., Gunaratne, P.H., Richards, S.W.,
Villalon, D.K., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and initial analysis of More than 15,000 full-length
human and mouse CDNA sequences
        4078 bp mRNA linear ROD 21-OCT-2003 Mus musculus cancer related gene-liver 1, mRNA (cDNA clone MGC:69583 IMAGE:6839525), complete cds.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314857. Location/Qualifiers
1. 4078
/organism="Mus musculus"
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                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 4078)
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Contact: MGC help desk
Email: cgapber-remail.nih.gov
Email: cgapber-remail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
EC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
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/clone="MGC:69583 IMAGE:6839525"
/tissue_type="Brain"
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vector_side:right"
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9 3412 GAAGTGTTCCTTCTGTTTCCTTTGTAATGTGATCCACTCGGGGAAATGGGTGTT 4519 by 2472 ACCAGGAAAATGTCCTCTCTCTCACCAGTCACCGGGGATCTGTTGAGGTGTT 4519 by 2472 ACCAGGAAAATGTCCTCTCCACCCCTACCAGGTCACTGTTTGTT	RESULT 5 AC120245 LOCUS LOCUS DEFINITION Rattus norvegicus clone CH230-259012, WORKING DRAFT SEQUENCE, 5 UNDOCACESSION AC120245 AC12024 AC120245 AC120245 AC120245 AC120245 AC120245 AC120245 AC120245 AC120245 AC12024
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Daylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:22856351.

The sequence in this sequence version replaced gi:22856351.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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Submitted (05-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 184163)
Rat Genome Sequencing Consortium.
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Center: Baylor College of Medicine
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REFERENCE

COMMENT

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12952 CTTGCCGCGTACCTGGGCTGCGTGTGCTTCGCTACTTCGATGCTGCCTCAGAGATACCC 13011
12892 GAGAAGCACTGCAGCACCCCGCTCACCCTCCCTTGCAGGCACATCCTCATCTGC 12951
                                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
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Best Local Similarity 77.3%; Pred. No. 0;
Matches 1886; Conservative 0; Mismatches 351; Indels 203; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 177885: contig of 177885 bp in length

886 179985: gap of unknown length

1986 179377: contig of 1392 bp in length

1981 179477: gap of unknown length

1978 180571: contig of 1094 bp in length

1972 180671: gap of unknown length

1973 18238: contig of 1855 bp in length

19336: contig of 1855 bp in length

19336: gap of unknown length

197463: contig of 1827 bp in length.

Location/Qualifiers
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CGTTTCTCGCTGTTTTTAGGGGATATGTGCTTCCTGAGTGACGTAGCCTCCCTAGGATG	14259 GAAGGGCAGACTCTGACTGAATGTCTCACCTGCACCATGCTGCTCCACTGGGCTA 14318 1962 TCTTCAGGGTATGAAGTGGGTATGGG-GTATCTCAGGGATGTTTGTAACTCAGGCACCTT 2020 14319 TCTGCAGGGTATGAGGTGGAATTGGGTATATCTCAGGGATGTTTGTAACTCAGGCACCTT 14378 2021 CTGCTTTCTGAGATTCCATTGTCAGTGATGTGTGTTTGTAACTCAGGGACTTGGAAC 2080 14379 CTGCTTTCTGACATTCCATTGTCAGGGAGAGGTGCAGCTCAGGGGACTTGGAAC 2080 14379 CTGCTTTCTGACATTCCATTGT-TGGGGTGGGGGACTCCAGGGGACTTGCTAC 14437 2081 ACCGTTCTGAGTGGTCCTGAAGGAGTGGGTACTGGGGACTTCTAGGACTTCTAGGG 2140		GGCTATTTCTTGTTTATAGTCACAAATATTTATAGACATGAAGGTGTAAAGATGTGTGTG	2377 TTGATTGCGATTTACAAGGCAGGAATACTTGGTTTTGATGATGATTATATGTCATTTTA 2436	2495 GITTATGGATGAGAGTGAGTCCTTTGGTTTTTGAGTCTAGAGTTTTCAGAGG 2554	2615 TATTCTACATAAGACTTATTATACATAAGTCTGTATAAATGTCCTGAAGATGACGCCTA 2674 14960 TATTCTACA	2729 GAACCCGTGTTGCTCTCCCCAGACGACCCAGCGACTTGTGAGGCTCAT 2777
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752 GAGCAAGGTCCAGTCATCAGATTCTGGCCCAGCGAAATGGGCTTTTATTGGTGTCCCT 811 13012 GAACAAGGTCCAGTCATCAGATTCTGGCCCAGTGAAATGGGCTTTTATTGGTGTCCCT 811 13012 GAACAAGGTCCAGTCATCAGATTCTGGCCCAGTGAAATGGGCTTTTATCGGTGTCCCC 13071 812 TATGTGTCCCTTCTGTGTGCCCACAAGAAGTCGCCAGTCAAGATCACGTGAAGGC 871 13072 TATGTGTCCTCCTGTGTGCCCACAAGAAGTCGCCAGTCAAGATCACGTGACGGCAAGGC 13131 872 AGTGACCAGCTTCTATTCTATTCGAGTGCCGCTGGGCTTTGCTAGCAA 931 13132 AGTGACCAGCTTTTCTATTCTATTCGAGTGTGCGCCTTTGTTTG	TTTG GGAC CATA CATA	1108 AGGRACATGACKAGAGTACTTGGGGACCCAAGGTTCTTGCTGGGG 1167 13372 ATGACATTGACAGGTAGTTTTTGGGACCCAGAGCCCAAGGTTTCTTGCTGGAG 1167 1168 AGGGTAGCTTGCTGTTTCCACCATTCTCACCCCAGAGCTTCTTGCTGGAA 13431 1168 AGGGTAGCTTGCTGTTTCCACCATTTCCAGACCCCTGATAAACAAGACC 1224	13492 C-CTGATTCTGTGATAGAAGTTCCAGAACTTTTCATTTTGCTGGGAGAAACTGTCCTTC	GGTGTGACTAAGACGGGTGGCTTGTCACTGGCACCTCTTAGGTTTCCCAGGTTCTCCACTCGCACTGGCTTCTCCACTGGCTTCTCCACTGGCTTCTCACTGGCTTCTCACTGGCTTCTCACTGGCTTCTCACTGGCTTCTCACTGGCTTCTCACTGCTGCTGCTGGCTG	AGCTGGCAACACCCTCTATGCCAAAAGCTACACTCTTTTAAGCACACTTACATAG	AIGHGAAGATTCCACACACACCCCTCTTGTGACCTCTGTGAGAGCAAGG -IGHGCAATTCCACACACACCCCTACCGCTTGCCACTTGACCTCTGTGAGAGCAAGG CTCGTTGTAATCGCGAAGGCAGCTCTG-GAGGCTTGACCTTGACGTCTGTGAGAGCAAGGCAGTTGAATTGACCTTGTGAAGAGCAGCTTGAATTGACCTTGAAGAGAGCAAGAGAGAG	1664 TIGG-AAAGCTTTCTTATTGGAAGCTTTTGGTGTTGTTGTTTGCTCCTCCTGTGAAGCT 1722 14020 TIGGAAAAGCTTTTCTTATTGGAAGCTTACAGTTGTTGTTGCTTACCTCCCAAGATTCTGACCC 1722 14020 TIGGAAAAGCTTTCTTATTGGAAGCTTACAGTGTTGTTACCTCCCAAGACTCTGACCC 14079

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Submitted (109-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON May 9, 2003 this sequence version replaced gi:24956965.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.func.edu/projects/rat/). Each config described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
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Consensus quality: 241576 bases at least Q40
Consensus quality: 243506 bases at least Q30
Consensus quality: 245010 bases at least Q30
Estimated insert size: 253391; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                    Direct Submission
Submitted (17-OCT-2001) Human Genome Sequencing Center, Departmer
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
           Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
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248565: gap of unknown length
249734: contig of 1169 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Baylor College of Medicine Center code: BCM
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Center project name: GAHA
Center clone name: CH230-3E15
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Rat Genome Sequencing Consortium.
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/db_xref="taxon:10116"
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                                     Weinstock, G. and Gibbs, R.A.
Direct Submission
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                                                                                                                                                    2 (bases 1 to 249734)
Worley, K.C.
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Standary, D. Marter, Marter, Abramacon, S., Adams, C., Alder, J., Allan, C., Allan, H., Alsbrooks, S., Amin, A., Anguiano, D., Allan, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Barbrooks, S., Anguia, A., Anguiano, D., Bandaranaike, D., Barber M., Barstsead, M., Benahmed, F., Biswalo, K., Blair, Y., Blair, D., Barber M., Barstsead, M., Benahmed, F., Biswalo, K., Blair, D., Barber M., Barstsead, M., Benahmed, F., Carcer, C., Cavazoe, I., Cener, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chan, R., Chen, Y., Chen, Y., Chen, Z., Chu, J., Chacko, J., Charez, D., Chan, R., Chen, Y., Chen, Y., Chen, Z., Chacko, J., Charez, D., Chan, G., Coyle, B., Din, H., Diva, K., Delang, S., Deramo, C., Ding, Y., Din, H., Diva, K., Delang, S., Finley, M., Flagg, N., Foster, M., Pester, F., Fanger, C., Barcho, S., Finley, M., Hamilton, K., Harvey, Y., Haviak, P., Hadan, S., Hadin, S.L., Hadgson, A., Hogsen, M., Harnadez, S., Finley, S., Haldun, S.L., Hodgson, A., Hogues, M., Howells, S., Hadun, S.L., Hang, J., Liu, J., Martin, R., Marti
15178 CATGCATGTGGTACACCTATGCATACAGGCAGGCAAGTCATTCGTACATGTAAAGT---- 15233
                                                                                                           2830 ---GCATTIGGIGCACACGIACATACAGGCAGACAATTIAIACAIGIAACGIAATA 2886
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus clone CH230-3E15, WORKING DRAFT SEQUENCE, 2
unordered pieces.
                                                                                                                                                                                                                                                                                                                    15234 AATGAGTAAGTTAATAAGCCGGCGGAGGGAAAGGTTTTTT 15273
                                                                                                                                                                                                                                                         2887 AATGCATAAGTTAGTGAGACGCCTGAAGGAAAGGAGTTTT 2926
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Ota,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamateu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Mateuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Takahashi-Ehiji,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., NeDO, human, cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-7UL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan (15-7UL-2004) Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human CDNA sequencing project supported by Ministry of Beconomy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); CDNA library
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens cDNA FLJ41587 fis, clone CTONG2020638.

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AK123581.1 GI:34529163

AK123581.1 Gi:34529163

AK100 capping; fis (full insert sequence).
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              GCTGCCTTTGTCTGAAAGGGCCCCGAGCTGTCTGGGGCTGGAAGCTGGTTCAGCCGATAA 151052
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 698 from Patent EP1440981.
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construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB, Incotation: HRI and RAB.
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/organism="Homo sapiens"
/organism="Homo sapiens"
/ml_type="mRNA"
/db_xref="taxon:9606"
/clone="CTONG2020638"
/tissue="type="tongue, tumor tissue"
/clone_lib="CTONG2"
/note="cloning vector: pME185FL3"
                                                                                                                                                                                                          17.3%; Score 722.2; DB 9;
Similarity 84.8%; Pred. No. 4.1e-184;
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Submitted (09-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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1 (Dases 1 to 14946).
Sulston,J.E. and Waterston,R.
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Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Jan 9, 2002 this sequence version replaced gi:14165368.
                                                                                                                                                                                                                                                                                                                                      CAAGAICACGIGAIGGCAAGGCAGIGACCAGCIICTCIACIIACIICTAIITCGAGIGCGC
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Homo sapiens BAC clone RP11-470J24 from 2, complete sequence.
AC017081
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RP11-470J24
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Contact: sapiens@watson.wustl.edu
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Genome Res. 8 (11), 1097-1108 (1998)
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Nguyen,C., Doebber,A. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone
Unpublished (2001)
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted:

o. MAPPING INFORMATION: Mapping information for this clone was provided by Dr. John

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21685. .21819
/rpt family="MIR"
22160. .22640
/rpt family="MER2_type"
22878. .23228
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7982. .8006
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3. .21566
_family="AT_rich"
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/rpt_family="(TATG)n"
.0320. .10341
                                                               /rpt_family="AT_rich"
8000. .8436
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/rpt_family="(TTG)n"
9685. .9973
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0333..10679
'rpt_family="AT_rich"
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21353. 21393
/rpt family="(T)""
/rpt family="(T)""
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|12707. .120c.
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16063. 17107
/rpt_family="L1"
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10681. 10757
/rpt family="L1"
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18177. 18501
/rpt_family="L1"
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8541. 8696
/rpt_family="L2"
8722. 9684
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/rpt_family="L1"
9378. .9422
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0280. .10305
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family="L1"
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2592. .12706
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family="L1"
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1999. .12591
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3139.
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10490.
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2966.
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                                                                              The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bapapac.med.buffalo.edu)
WECTOR: DRACG3.6
WEIGHBORING SEQUENCE INFORMATION:
     Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1127. 1561
/note="match to EST AA056210 (NID:g1548612) zf62g06.s1"
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                                                                                                                                                                                                                                           The clone sequenced to the left is RP11-310K15, 2000 bp overlap: the clone sequenced to the right is RP11-156A1, 2000 bp overlap. Actual start of this clone is at base position 190775 of RP11-310K15; actual end is at base position 28935 of RP11-156A1.
McPherson, Department of Genetics, Washington University, St. I
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                        The sequence between 81601 and 81703 is covered only by a pcr product of clone DNA. Unresolved tandem repeat regions exist between 81548 and 83183, 126196 and 127426.

Location/Qualifiers
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2991. .3324
/note="match to EST R35058 (NID:g791959) yh86d09.rl"
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/note="match to EST AW452004 (NID:g6992780)"
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| Organism="Homo sapiens"
| Mol type="genomic DNA"
| db xref="taxon:9606"
| chromosome="2"
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/rpt_family="GC_rich"
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141. .282
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822 Dp DNA linear ent W00155408.	rtebrata; Eute Hominidae; Hom	Memorec Medical Molecular Research Cologne Stoffel GmbH (DE) FEATURES Location/Qualifiers 1. 822 1. 822 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match Query Match Best Local Similarity 87.9%; Pred. No. 1.3e-165; Matches 725; Conservative 0; Mismatches 97; Indels 3; Gaps 1;	Oy 35 ATGGGCCCCGCACTGGTGGGACCACCTGCGGGCTGGCAGTTCGGAGGTGGATTGGTGC 94	Qy 95 GAGGACAACTACACTATCGTGCCTGCCATTGCCGAGTTCTACAACACGATCAGCAACGT 154	QY 155 TTGTTTTCATTTTACCTCCCATCTGCATGTGCTTGTTCCGCCAGTACGCAACGTGCTTC 214	Qy 215 AACAGGGGATCTACTTAATATGACGCTCCTAGTTGTAGTGGGGATTGGATCTGTCTAC 274	OY 275 TICCAIGCAACGCTGAGTTTCCTGGGTCAGATGCTTGATGAACTTCTGTGGGTT 334 Db 238 TICCAIGCAACCTTAGTTTCCTGGGTCAGATGCTTGAIGAACTTGCAGTCTTTGGGTT 297	Qy 335 CTGATGTGTGCCATGTGGTTTCCCAGGAGGTATTACCAAGGACTTTCGGAAT 394 Db 298 CTGATGTGTGCTTCGGTCATGTGGTTCCCCAGAAGGTATCTACCAAAGGTCTTTCGGAAT 357	Qy 395 GACAGGGCAGGTTCAAGGCAGTGGTGTGTCTGCTGCAATTACAACGTGCTTGGCG 454	OY 455 TTTATCAAGCCGGCATCAACAATATTTCCCTGATGATTCTGGGACTTCCATGCACTGCG 514	Qy 515 CTGCTTGTTGCAGAGCTGAAGAGGTGTGACAATGTGCGTGTGTTAAGCTGGGCCTCTTC 574	QY 575 ICTGGCCTCTGGTGGACTCTGGCTGCTGGATCAGCGACCAAGCTTCTGTGAG 634	Oy 635 CIGCICCTCCTTCACTTCCCCTACCTGCACTGTGGGCATATTCTCATCTGCCTT 694	Qy 695 GCTTCGTACCTGGGCTGTGTGTCTTCGCCTACTTTGATGCTGCCTCAGAGATACCTGAG 754
Query Match 16.9%; Score 705; DB 9; Length 149462; Best Local Similarity 84.4%; Pred: No. 2.7e-179; Addisonal Similarity 84.4%; Pred: No. 2.7e-179; Matches 818; Conservative 0; Mismatches 145; Indels 6; Gaps 2; QV 10 GCTGCTCCGATGCTCCAGAGCGCCCTGCGCCCCCGCACTGCTGCAGGC 69 Db 136946 GCTGCTCCCAATGCCCCAGAGTGGCCCCCCGCACTGCTGCAGGC 136887 QY 70 TGCAGTTCGAGAGTGGATTGGTGCAGAGAACTACACTATGCTGCCCATTGCCGA 129 QY	Db 136886 TGGCAGCTCGGAACTGGCGCAGAGTTACACTTCGTCGTCGTGTTGTGTGTG	190 136766 250	Db 136708 TGTAGCGGGAATTGGATCCGTCTACTTCCATGCAACCCTTAGTTTCTGGGTCAGATGCT	GTCCT GTCCT	OY 430 GTCTGCAATTACAACGTGCTTGGCGTTTATCAAGCCCGCCATCAACAATATTTCCCTGAT 489	AATGT 549 	Qy 550 GCGTGTGTTTAAGCTGGCCTCTTCTCTGGTGGACTCTGGCTCTTCTGCTG 609 Db 136408 GCGTGTTTAAGCTGGGCCTCTTCTCGGGCCTCTGGTGACCCTGGCCCTGTTCTGGTG 136349		Qy 670 IGIGIGGCATATICICATCTGCTIGCTICGTACCTGGGCTGTGTGCTICGCCTACCT 729		CCAGT 	909	910 GCTGGGCTTCGTTTGCTAGCAAAGATGGCTGAGGGGGTTGAGGAATTGGTGTGGTGGGG 136052 AGTGGGCTTTGCTTTGGTAGGAAGATGAGCTAAACAAATTCAAAAAAAA	970 TGTTTAAA 978	00000 111111 300000

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PAT 06-JUN-2002
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                      241 GTAGAGGGCTCAGGGACATAAGGTGTCTTCCTCAGTATCCTTTCCAGGCATACGGGCTTG
                                                                                                                                                                                                                                                                                                     421 CCTGATAAACAAGACCTTCTGATTTGGTGATGAAAGGTTCCAGAACTTTTCATTTTGCCG
                      TITAAAAITCIGCICCITIGIGAICIAACIGGACCACIGIGCCIGACCICCCIAGGIIAA
                                            181 TITAAAAITCTGCTCCTTTGTGATCTAACTGGACCACTGTGCCTGACCTCCCTAGGTTAA
                                                                                                                                                                                                                                    301 creserrargrecarargacaccaacagagragrecrrressagaccrassecaacca
                                                                                                                                                                                                                                                                                                                                                                 1209 CCTGATAAACAAGACCTTCTGATTTGGTGAAAGGTTCCAGAACTTTTCATTTTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3557 ATTCTATTGGTTGGATTTCTCAGGAGTCTGAATCTTCCCTCACGAGTCCTCTTCTCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGCCTCCCAGATC---CACTGGGATTTGAACCTTCAAATCCTGCCTCTTCTTCTTCTTC
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                                                                                                                                                                                         CTGGGTTATGTCCATAATGACATCAACAGAGTAGTTCTTTGGGAGACCTAGGGCAACCCA
                                                                                                                                                                                                                                                                              1152 AAGTITCTTGCTGGAGAGAGATAGCTTGCTGT---TTCCACCATTTCCAGACTCTCAACCC
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Molecular toxicology modeling
Patent: WO 0210453-A 119 07-PEB-2002;
Gene Logic, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
9.6%; Score 400.4; DB 6; Length 595;
Best Local Similarity 87.9%; Pred. No. 7.8e-97;
Matches 531; Conservative 0; Mismatches 56; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="unassigned DNA"
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WO0210453.
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Sequence 119 from Patent
AX400443
AX400443.1 GI:21336623
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AX400443/c
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AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as STSs and 81,000 SNPs were annotated with alleles from CS7BL/6J and the Strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AGATCACGTGATGGCAAGGCAGTGACCAGCTTCTCTACTTCTATTCGAGTGCGCGC 120
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GCTGCCTACCTGGGCTGTGTATGCTTTGCCTACTTTGATGCTGCCTCAGAGATTCCTGAG 717
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                                                                                                                                                                                                                                                                              G76816 S208P6606FG12.T0 129S1/SvImJ Mus musculus STS genomic, sequence
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                                                                       CAAGGTCCAGTCATCAGATTCTGGCCCCAGCGAGAAATGGGCTTTTATTGGTGTCCCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Whitehead Institute for Biomedical Research, Center for Genome
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                                                                                                                               GIGTCCCTTCTGTGCCCACAGAAGTCGCCAGTCAAGATCACG 859
                                                                                                                                                        778 GIGICCCICCIGIGIGICAACAAGAAATCAICAGICAAGACCACG 822
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/organism="Mus musculus"
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/clone lib="12951/Sv1mJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 Charles Street, Cambridge, MA 02141, USA Tel: 6172521477
Fax: 6172580903
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Pred. No. 8.4e-127;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphism Structure in the Mouse Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; 'Mammalia; Butheria; 'I (bases 1 to 531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kerstin Lindblad-Toh
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Best Local Similarity 99.1%;
Matches 525; Conservative 0
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Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGATCAGCGACCAACCATCTGTGAGCTGCTCTCCTTTCACTTCCCCTACCTGCACT 668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                      784 ACCTGGGTGCTGTTGGTCCCACTGGCCAACAACACATCTTTGGCCAGATTGGGATTCTCA
                                                                                                                                                                                                                                                                                             3827 ATAGATITIATAGACATTATTCTCCCACAGACTTTAAAACATGGCTTGTGTCTTTCCATA
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                                                                                                                                                                                                       3767 ACCTGGGTGCTGTTGGTCCCACTGGCCAACACACATCTTTGGCCAGATTGGGATTCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 TTTATGCTTTTTTGGAACTCTGATAACCATGGTCAATATTAAAGCCATTAACTGGCATT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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         /map="- 4 22-692 84245395-84244718"
/clone lib="CZECHII/Ei"
<1. .>784
                                                                                                                        DB 11;
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                                                                                                                   Score 382.6; DB 1
Pred. No. 5.4e-92;
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PE Corporation (NY) (US)
Location/Qualifiers
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89.5%; Pred. No. 4.5e-59;
iive 0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CQ736905 315 bp DNA Sequence 22839 from Patent WO02068579. CQ736905
                                                                                                        9.2%; Sco...
99.0%; Pred. No. 5...
... 0; Mismatches
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 89.5'
Matches 281; Conservative
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CQ736905
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Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C., Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
                                                                                                                                                       3910 ATTITATAACCACAGGAATTAAAACCAAGCAAATAGAGTACTTTCAGATATAAACTGTGTT 3969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               65
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CACAGACTTT - - AAAACATGGCTTGTGTTTTCCATACACATCCGGTCAGATTTAAAACT
                                                                                                                                                                                                                                                                                    183 TTATACTTTATGTAGAGTGTGCTATGTACAGGTGGCATGTACCCTGGCTGAGGTAACATT
                                                                                                                                                                                                                                                                                                                                                          123 AGTCATTGCTCTGGG-GGATTTACAGATCTTTTGCACTTTATGCTGAACTCT
                                                                                                               298 CACAGACTITAAAAAACATGGCGTGTGTCTTTTCCTACACA---AGTCAGATTTAAAACT
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Whitehead Institute for Biomedical Research, Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BV053534 170 CZECHII/Ei Mus musculus STS genomic, sequence
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/organism="Mus musculus"
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/strain="CZECHII/Ei"
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Fax: 6172580903
Email: kersli@genome.wi.mit.edu
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Primer B: None
STS size: 784
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RESULT 13 BV053534/c

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE PUBMED COMMENT

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788
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Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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                                  728
                                              GCATGEGGCACATCCTCATCTGCCTTGCTTACCTGGGCTGTGTATGCTTTGCCTACT 181
                                                                                                          182 TTGATGCTGCCTCAGAGATTCCTGAGGAGCCCTGTCATCAAATTCTGGCCCAGCGAGA 241
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62 GGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCAACTTCCCCTACCTGCACT 121
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                            669 GIGIGIGGCAIAITCICAICIGCCIIGCIICGIACCIGGGCIGIGIGIGGGIICGCCIACI
                                                                                          TTGATGCTGCCTCAGAGATACCTGAGCAAGGTCCAGTCATCAGATTCTGGCCCAGCGAGA
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PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       CQ736906 315 bp DNA Sequence 22840 from Patent WO02068579. CQ736906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Matches 281; Conservative
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Acc50961 Human bla
Adn38833 cancer/an
Abs54149 Human cDN
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Adl06640 Human 3T3
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Ab130432 I
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                  hits satisfying chosen parameters:
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ALIGNMENTS

Novel polypeptide designated as CRG-L1, useful as diagnostic marker for liver cancer, is differentially expressed in liver tumors relative to normal liver tissues. The invention relates to a polypeptide designated as CRG-L1), which is differentially expressed in liver tumours relative to normal expression Location/Qualifiers
35. .8a /*tag= a /product= "Liver tumour marker protein, CRG-L1" Mouse cDNA encoding a liver tumour marker protein, CRG-L1. Mouse, ss, gene, liver cancer, liver tumour, CRG-L1, hepatocellular cancer. Claim 2; Page 4-7; 11pp; English. ABSS4148 standard; cDNA; 4175 BP. 14-DEC-2001; 2001US-00017410. 14-DEC-2000; 2000US-0255674P. (first entry) farnham PJ, Graveel CR; (FARN/) FARNHAM P J. (GRAV/) GRAVEEL C R. WPI; 2002-706409/76. P-PSDB; ABG32880. US2002115094-A1. Mus musculus 22-AUG-2002.

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in normal liver tissues, designated CRG-Li. Also included are the encoding polymuclectides (in the case of the human sequence, mapping to chromosome Sp), expression constructs, host cells, anti-CRG-Li antibodies, identifying modulators of CRG-Li, and the use of the CRG-Li sequence in the diagnosis of hepatocellular cancer in tumour cells from liver of a human or non-human animal. The CRG-Li protein and polymucleotide are useful as diagnostic markers for a liver cancer in humans and non-human animals, and as a system for assessing putative therapeutic agents. The present sequence encodes mouse CRG-Li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
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03-AUG-2001, 2001US-0310099P.
08-NOV-2001, 2001US-0343705P.
13-NOV-2001, 2001US-0350666P.
12-APR-2002, 2002US-0372246P.
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13-NOV-2002;
              Homo sapiens
                                  03-DEC-2001;
14-DEC-2001;
                                                  04-APR-2002;
12-APR-2002;
                                      08-JAN-2002;
                                            13-FEB-2002;
20-FEB-2002;
                                                29-MAR-2002;
                                                     05-JUN-2002;
                                                                     D,
DH,
                                                                 (EOSB-)
                                                                       Mack
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fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jish KC, Glynne R, Hevezi PA;
Wilson KE, Zlotnik A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 151; 1385pp; English.
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R, Watson SR,
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2001US-0334393P
2001US-0334394P
2001US-0347211P
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2002US-0357349P
2002US-0357344P
2002US-0356714P
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2002US-0397845P.
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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.

The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
the diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
also be useful in wound healing and un contraception. The present sequence represents a nucleic acid sequence of the invention

Sequence 4212 BP; 1047 A; 894 C; 932 G; 1339 T; 0 U; 0 Other;

4 17.3%; Score 723.8; DB 11; Length 84.9%; Pred. No. 5.5e-189; vative 0; Mismatches 142; Indels Query Match
Best Local Similarity 84.94
Matches 823, Conservative

10 GCTGCTCCGATGCTCCAGAGCGGCCATGGGCGCCCCGCACTGGTGGGACCACCTGCGGGC

189 249 301 309 369 429 958 AGTGGGCTTCCTTTGCTAGGAAGACAGCCAAGGGAGTTCGAATAGTTGGGGTTGTGGGCTA 1017 361 481 489 541 609 699 601 661 721 729 781 789 841 CAAGATCACGTGATGGTGGTGGTGGCTTCTTCTGTTATCGCCCTC----ATGC 957 GCTGGGCTTCGTTTGCTAGCAAAGATGGCTGAGGGGGTTGAGGAATTGGTGTGGTGTGGG 969 TGATGAACTIGCCAITCTGTGGGTTCTGATGTGTGTTTTGGCCATGTGGTTTTCCCAGGAG 250 TGTAGTGGGGATTGGATCTGTCTACTTCCATGCAACGCTGAGTTTCCTGGGTCAGATGCT 242 GTTTCGTCAGTATGCAACATGCTTCAACAGTGGCATCTAACTTAATCTGGACTCTTTTGGT GATTCTGGGACTTCCATGCACTGCGTTGTTGCAGAGCTGAAGAGGTGTGACAATGT 602 degratariana de concercio de concentra de consecuencia de GATCAGCGACCAAGCCTTCTGTGAGCTGCTCTCCTCTTTCACTTCCCCTACCTGCACTG GTCTGCAATTACAACGTGCTTGGCGTTTATCAAGCCCGCCATCAACAATATTTCCCTGAT GTCTGCGGTTACGACGTGCCTGGCATTTGTCAAGCCTGCCATCAACAACATTTTCTCTGTAT 542 GACCCTGGGAGTTCCTTGCACTGCTCATCGCAGGGCTAAAGAGGTGTGACATT GATCAGTGACCGAGCTTTCTGCGAGCTGCTGTATCCTTCAACTTCCCCTACCTGCACTG CAIGIGGCACATCCTCATCTGCCTTGCTGCCTACCTGGGCTGTGTATGCTTTGCCTACTT TGATGCTGCCTCAGAGATACCTGAGCTCCAGTCATCAGATTCTGGCCCAGCGAGAA TGTTTAAAA TCTTTTCAA 62 70 190 310 362 370 422 430 482 490 550 510 662 722 730 782 790 842 902 850 g à g q ò à g ò d à q ò d g g Š à ò g à g a à ઠે g à ద Š 8

standard; cDNA; 828 BP. ABS54149 ABS54149; ABS54149 ID ABS5 XX AC ABS5 RESULT

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GACAGGGTAGGTTCAAGGTGGTCAGTGTCCTGTCTGCGGTTACGACGTGCCTGGCA 420
241 TTCCATTITACCCTTAGTTTCTTGGGTCAGATGCTTGATGAACTTGCAGTCCTTTGGGTT 300
                                                                                                Ceramidase; human; K3; antiproliferative; anticancer; anti-eczema; antipsoriasis; dermatclogical; ceramide; sphingosine; treatment; ds; altered cell proliferation; cancer; neurodermatitis; eczema; cosmetic; permeability barrier; psoriasis; ichthyosis; lamellar ichthyosis ICR2.
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09-MAR-2000; 2000DE-01011392.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a polypeptide designated as CRG-LII), which is differentially expressed in liver tumours relative to normal expression in normal liver tissues, designated CRG-LII. Also included are the encoding polymucleotides (in the case of the human sequence, mapping to chromosome 9p), expression constructs, host cells, anti-CRG-LI antibodies, identifying modulators of CRG-LII, and the use of the CRG-LII sequence in the diagnosis of hepatocellular cancer in tumour cells from polymucleotide are useful as diagnostic markers for a liver cancer in humans and non-human animal: The CRG-LII protein and humans and non-human animals, and as a system for assessing putative therapeutic agents. The present sequence encodes human CRG-LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polypeptide designated as CRG-L1, useful as diagnostic marker for liver cancer, is differentially expressed in liver tumors relative to normal liver tissues.
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1. .828
/*tag= a
/product= "Liver tumour marker protein, CRG-Ll"
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Pred. No. 4.7e-173;
0; Mismatches 102; Indels 0
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                                                                                                               Human cDNA encoding a liver tumour marker protein, CRG-L1.
                                                                                                                                                               Human, 88; gene; liver cancer; liver tumour; CRG-L1; hepatocellular cancer; chromosome 9p.
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Best Local Similarity 87.7%;
Matches 726; Conservative
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                                                         (first entry)
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Conradt M;

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2001-483256/52
    P-PSDB; AAB86365
Hofmann K,
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This invention describes novel human ceramidase (I) containing a specific structural motif which has antiproliferative, anticancer, anti-eczema, antipsoriasis and dermatological activity. (I) cleave ceramide, resulting in formation of sphingosine. (I) or the nucleic acid (II) encoding it, are used for diagnosis, prevention or treatment of diseases associated with ceramide defects, particularly altered cell proliferation (cancer) psoriasis), also for targeted modification of the permeability barrier by ceramidase or its activators, e.g. for transcutaneous delivery of substances. Specifically they are used for diagnosis of ichthyosis, particularly lamellar ichthyosis ICR2. (I) can also be used in cosmetics. This sequence encodes human ceramidase X3 New ceramidase containing specific structural motif, useful for diagnosis, prevention and treatment of ceramidase defects, e.g. ichthyosis, also in cosmetics. Claim 3; Page 17; 31pp; German.

Sequence 822 BP; 153 A; 225 C; 209 G; 235 T; 0 U; 0 Other;

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154 120 214 180 274 237 514 TICCAIGCAACGCIGAGIIICCIGGGICAGAIGCIIGAIGAACIIGCCAIICIGIGGGII 334 297 CTGATGTGTGCTTTTGGCCATGTGGTTTTCCCAGGAGGTATTTACCAAAGATCTTTCGGAAT 394 GACAGGGGCAGGTTCAAGGCAGTGTGTGTGTCTGTCTGCAATTACAACGTGCTTGGCG 454 daccaddoraddricaaddrodrodroricrororocagriaradacorocadda 417 TrigicaAgcicidecarcaacaacricicardaardaccirogaagriccriocacidea 477 574 537 634 597 94 9 694 657 ATGGGCCCCCGCACTGGTGGGACCACCACACAGGTGGCAGCTCGGAGGTGGACTGGCGC 61 GAGGACAACTACATCGTGCCTGCTGTCGCGGAGTTCTATAACATGATCAGCAATGTC 121 Tratititicatititaccecccatciecaretecriciticicacianicalecaretec 215 AACAGCGGCATCTACTTAATATGGACGCTCCTAGTTGTAGTGGGGGATTGGATCTGTCTAC ATGGGCCCCCCCACTGGTGGGACCACCTGCGGGCTGGCAGTTCGGAGGTGGATTGGTGC GAGGACAACTACACTATCGTGCCTGCCATTGCCGAGTTCTACAACACGATCAGCAACGTC TIGITITICATITITACCICCCATCIGCATGIGCTIGITCCGCCAGIACGCAACGIGCTIC Aacadcigicatichachtaanchg---gchchrightaragcagaahhagahccanchac Trccarccaacccrractrrccressicaarscrraarsaacrracarccrrisserr TTTATCAAGCCCGCCATCAACAATATTTCCCTGATGATTCTGGGACTTCCATGCACTGCG 538 rcadacercradadeceradecerarieracidareadadecadecrireracidade Gaps CTGCTTGTTGCAGAGCTGAGAGGTGTGACAATGTGCGGTGTTTAAGCTGGGCTCTTC TCTGGCCTCTGGTGGACTCTGTTCTGCTGGATCAGCGACCAAGCCTTCTGTGAG 635 CIGCICTCCCCTITCACTICCCCTACCIGCACIGIGIGGGALATICICALCIGCCTI 3; 97; Indels Score 653.8; DB 4; Pred. No. 5.3e-170; 0; Mismatches 15.7%; Query Match
Best Local Similarity 87.9°
Matches 725; Conservative 35 Н 95 155 181 275 238 335 298 395 358 418 515 478 575 455

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The invention relates to an isolated polymucleotide encoding a polypeptide with biological activity. The polymucleotides and polypeptides are useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polymucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in corresponding polypeptide is expressed, for neve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents cDNA encoding a novel human protein. 717 814 GCTTCGTACCTGGGCTGTGTGTGCTTCGCCTACTTTGATGCTGCCTCAGAGATACCTGAG 754 777 forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; bone cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue repair; tissue replacement; burn; incision; ulcer; cancer; human; New polynucleotides and secreted proteins, useful for treating myeloid or tymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement. Wang J; Wang D; 658 écigéciaccidescrigitatiscririsceraciridatiscrescricasatirecrisas CAAGGTCCAGTCATCAGATTCTGGCCCAGCGAGAATGGGCTTTTATTGGTGTCCCTTAT 718 CAAGGCCTGTCATCAAATTCTGGCCCAGGGAAATGGGCCTTCATTGGTGTCCCCTAT J, Zhao QA, Drmanac RT, 815 GIGTCCCTTCTGTGTGCCCACAGAAGTCGCCAGTCAAGATCACG Goodrich RW, Ren F, Zhang Wehrman T, Weng G, Zhou P, Claim 1; SEQ ID NO 207; 156pp; English. ADI21948 standard; cDNA; 1623 Novel human protein cDNA #207. 19-SEP-2002; 2002WO-US029964. 19-SEP-2001; 2001US-0323739P. 13-SEP-2002; 2002US-00323739. (first entry) Tang YT, Asundi V, Ghosh M, Xue AJ, W Haley-Vicente D; 2003-354603/33 (HYSE-) HYSEQ INC P-PSDB; ADI21232 WO2003025148-A2. Homo sapiens. 15-APR-2004 27-MAR-2003 695 755 ADI21948; ò 엄 셤 à

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differential expression; centrilobular necrosis; steatosis.
                                                                                                     4.
                                                              DB 10; Length 1623;
                        U; 0 Other;
                                                                                                   Indels
                                                          Score 424.2; DB 10;
Pred. No. 3.3e-106;
0; Mismatches 113;
                        Sequence 1623 BP; 305 A; 457 C; 382 G; 479 T; 0
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                                                              Query Match
Best Local Similarity 81.2%;
Matches 506; Conservative
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compounds or the progression of these court ellects by determining the global changes in gene expression in tissues or cells exposed to the coupling these to gene expression in unexposed tissues or toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or expression in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The casponse and predict cellular pathways that a compound modulates the toxic response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer specifically hybridises to a gene listed in the specification, of expression level in a tissue or cell sample exposed to a hepatotoxin of system comprising at least two genes listed in the specification, cell rapide expression level in a tissue or cell of at least one gene changes in gene expression and for identifying toxicity markers in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in the proper control of the probes of the pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence tag (EST) or cDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the
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9.6%; Score 400.4; DB 6;
Best Local Similarity 87.9%; Pred. No. 7.2e-100;
Matches 531; Conservative 0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Castle AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 119; 239pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnson KR,
02-NOY-2000; 2000US-0244880P.

11-MAY-2001; 2001US-0290645P.

15-MAY-2001; 2001US-0290645P.

22-MAY-2001; 2001US-0295798P.

06-UUN-2001; 2001US-0295798P.

13-UUN-2001; 2001US-0297457P.

19-UUN-2001; 2001US-0298848P.

09-UUL-2001; 2001US-0303459P.
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of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect of a compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

DB 10; Length 595;

Sequence 595 BP; 197 A; 101 C; 146 G; 151 T; 0 U; 0 Other;

ftp.wipo.int/pub/published_pct_sequences.

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                                                                  CACAGACTIT -- AAAACATGGCTTGTGTCTTTCCATACACATCGGTCAGATTTAAAACT
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                            CCAACAACACATCTTTGGCCAGATTGGGATTCTCAATAGATTTTTATAGACATTATTCTCC
                                                                                                                         241 ATTTTATAACTACAATAATTCAACCAAGCAAATAGAGTATTTCAGATATATGC--CATT
                                                                                                                                                                                                   123 AGTCATTGCTCTGGG-GGATTTACAGATCTTTTGCACTTTATGCTTTTTTTGTGAACTCT
                                                                                                                                                                                                                                        GATAACCATGTTCAATATTAAAGCCATTAACAGGCATTTTCTGTGAATAAACATTTATGT
                                                                                                                                                                                                                                                                                                                                                                                                          expression profile; hepatotoxicity; liver;
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drug screening; toxicity assay; ds.
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                                                                                                                                                                CCAGCCAAACTTGGATTCTTCCCAACCAGGCTTGACCTGGGTGCTGTTGGTCCCACTGC
                                                                                               3617 CCCCTACCCAGAGCCAACACTGGGATTTGAACCTTC----TCTGACTCTCTTCTTCCCTC
                                                                                                                                                                                                                                                                595 ATTCTATTGGTTGGACTTCTCAGGTGTCTGAAACTTCCCTCAGGAATCCTCTTCTCCTAA
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                         Indels
                         26;
 Score 400.4; DB 10
Pred. No. 7.2e-100
                        0; Mismatches
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Query Match
Best Local Similarity 87.9%;
Matches 531; Conservative
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Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.

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Elashoff

Castle A,

'n Higgs

Johnson K,

Porter M,

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Mendrick

WPI; 2003-689530/65.

The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile

Claim 1; SEQ ID NO 252; 1156pp; English.

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promoting function, polynucleotides encoding the polypeptide and the recombinant process of producing the polypeptide. The present invention also discloses the agonist resisting the polypeptide and its treatment effect. The present invention also discloses the application of the polynucleotides encoding the human protein with 3T3 cell conversion
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                                                                                                                                                                 -AGGIGIGACAAIGIGCGIGIGITITAAGCIGGGCCICTICICIGGCCICI
                                                                    658 GACCCCCGTGCAGGTGTGACAACATGCGTGTTTTAAGCTGGGCCTCTTCTCGGGCCTCT
                                                                                                                             CITCTICTGCTGGATCAGCGACCAAGCCTTCTGTGAGCTGCTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein with function of promoting 3T3 cell conversion and its
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                                                                                                                                                                                                                                                                                                    823
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                                                                                                                                                                                                                                                                               CCTTTCACTTCCCCTACCTGCACTGTGTGGCATATTCTCATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 3T3 cell conversion promoter PP11646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoting function, polymucleotides encoding the polypeptide and the recombinant process of producing the polypeptide. The present invention also discloses the agonist resisting the polypeptide. The present invention affect. The present invention also discloses the application of the polymucleotides encoding the human protein with 3T3 cell conversion promoting function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conversion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 1527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel human protein with 3T3 cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1527 BP; 376 A; 357 C; 383 G; 411 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 323.6; DB 10;
Pred. No. 2.4e-78;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHAN-) SHANGHAI XINSHIJIE GENE TECHN DEV CO LTD.
                                                        Human 3T3 cell conversion promoter PP11646 cDNA
                                                                                                              cell conversion; promoter; human; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCATGCACTGCGCTGCTTGTTGCAGAGCTGAAG
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                                                                                                                                                                                                                                                                                                                                              12-SEP-2001; 2001CN-00126725
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                                                                                                                                                                          Homo sapiens
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06-MAY-2004
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                                                                                                                                                                                                                                                                                                                                                                                              forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; none cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue repair; tissue replacement; burn; incision; ulcer; cancer; human; ss; gene; EST; expressed sequence tag.
                                              TGGATCCGTCTACTTCCATGCAACCCTTAGTTTCTTGGGTCAGATGCTTGATGAACTTGC
                                                                       CATTCTGTGGGTTCTGATGTGTGCTTTGGCCATGTGGTTTTCCCAGGAGGTATTTACCAAA
                                                                                       AGTCCTTTGGGTTCTGATGTGTGCTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAA
                                                                                                                       GATCTTTCGGAATGACCGGGGTAGGTTCAAGGTGGTCAGTGTCCTGTCTTGCGGGTTAC
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                                                                                                                                                                                                                                                                                                                                            558 GACCCCCGTGCAGGTGTGACAACATGCGTGTGTTTAAAGCTGGGGCCTCTTCTCGGGCCTCT
                        TGGATCTGTCTACTTCCATGCAACGCTGAGTTTCCTGGGTCAGATGCTTGATGAACTTGC
                                                                                                                                                                         AACGTGCTTGGCGTTTATCAAGCCCGCCATCAACAATATTTCCCTGATGATTCTGGGACT
                                                                                                                                                                                           478 GACGIGCCIGGCATITGICAAGCCIGCCAICAACAACAICTCICIGAIGACCCIGGGAGI
                                                                                                                                                                                                                                                                                                                            - AGGIGTGACAAIGTGCGIGTGTTTAAGCTGGGCCTCTTCTCTGGCCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao QA,
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ou P, Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human expressed sequence tag, EST #167.
                                                                                                                                                                                                                         TCCATGCACTGCGCTGCTTGTTGCAGAGCTGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YI, Asundi V, Goodrich RW,
Ghosh M, Xue AJ, Wehrman T, Wen
Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВЪ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI21468 standard; cDNA; 487
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13-SEP-2002; 2002US-00323739
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The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in corresponding to the mound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents a novel human expressed sequence tag, EST.
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                                                 polynucleotides and secreted proteins, useful for treating myeloid or
                                                                 lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 487 BP; 81 A; 138 C; 131 G; 134 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.1%; Score 294.8; DB 10; Length Best Local Similarity 89.5%; Pred. No. 1.2e-70; Matches 317; Conservative 0; Mismatches 37; Indels
                                                                                                                                      Example 2; SEQ ID NO 719; 156pp; English.
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2003-354603/33
              P-PSDB; ADI21688
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ao QA, Wang D, Wang J, Zhang J, Ren F,
Yang Y, Wejhrman T, Goodrich R;
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, Yang Y,
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Xue AJ,
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                                                                                                                                                                                                                                                                                                   BP.
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09-MAR-2000; 2000DE-01011392
                                                                                                                                                                                                                                                                                                 AAH48639 standard; DNA; 792
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                                                                                                                                                                                                                              917 GICAGGACTIGC 928
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                                                                                                                                                                                                   914 GGCTTCGTTTGC
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                                                                                                                                                The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to oytokine, cell prollferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, insure growth factor activity, immunomodulatory activity and activity, insure constructs, leaves activity, and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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                                                                                 Nucleic acids encoding polypeptides with cytokine-like activities, useful
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  Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 412; Indels
  Ren F,
  Wang J, Zhang J,
1 T, Goodrich R;
                                                                                                                       Claim 1; Page 4462; 6221pp; English.
  Wang D, Wan
Wejhrman T,
                                                                                                diagnosis and gene therapy
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                                        WPI; 2001-476283/51.
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 hao QA, I
Yang Y,
                                                      P-PSDB; AAM79417
 Zhao
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Matches 437;
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739
                                                                                                                                                                                                                                                                                                                                                                                          856
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                                                                                                 GCTGCCTCAGAGATACCTGAGCAAGGTCCAGTCATCAGATTCTGGCCCAGCGAGAAATGG
                                                                                                                                                                                        GCCAACTATGAGATGCCAGGTGAAACCCTCAAAGTCCGCTACTGGCCTCGGGACAGTTGG
                                                                                                                                                                                                                                                                                         794 GCTTTTATTGGTGTCCCTTATGTGTCCCTTCTGTGTGCCCACAAGAAGTCGCCAGTCAAG
                                                                                                                                                                                                                                                                                                                                                                                          CC---CGTGGGGCTGCCCTACGTGGAAATCCGGGGTGATGACAAGGACTGCTGAGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New ceramidase containing specific structural motif, useful for diagnosis, prevention and treatment of ceramidase defects, e.g. ichthyosis, also in cosmetics.
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529 CÁGAGGT 535
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                                                                             TACAACACGATCAGCAACGTCTTGTTTTTTTTTTTACCTCCCATCTGCATGTGCTTGTTC 193
                                                                                                85 TACAACACGTTCTCCAATATCCCCTTCTTCATCTTCGGGCCACTGATGATGCTCCTGATG 144
                                                                                                                                        145 CACCCGTATGCCCAGAAGCGCTCCCGCTACATTTACGTTGTCTGGGTCCTCTTCATGATC 204
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                     Gaps
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pharmaceutical; gene; ds.
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 Length
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DB 4;
Score 174.8; DB 4;
Pred. No. 2.8e-37;
0; Mismatches 342;
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 4.2%;
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        al Similarity 52.6
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23-MAR-2001; 2001WO-US009231.
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Sequence 14, Application US/08232463
; Betent No. 5670367
; GENERAL INFORMATION:
APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALMER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESSENENCE FOLSY, Lardner
; ADDRESSEE: FOLSY, Lardner
; STREET: 1800 Diagonal Road, Suite 500
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Matches 122; Conservative
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US-09-621-976-11241
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US-09-621-976-11241/c
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LENGTH: 358
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US-08-232-463-14
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                                                                                                                                                            (without alignments)
8308.591 Million cell updates/sec
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                                                                                                                                                                                                                                                                              November 20, 2004, 20:51:27; Search time 357.166 Seconds
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-621-976-11241
US-08-232-463.14
US-09-790-421-14
US-09-790-421-14
US-09-621-976-2813
US-09-621-976-2813
US-09-621-976-2813
US-09-621-976-2813
US-09-644-796-17
US-09-244-796-17
US-09-48-7968-16
US-09-48-7968-16
US-09-49-406-1
US-09-49-406-1
US-09-49-406-1
US-09-49-406-1
US-09-327-138C-38
US-09-327-138C-38
US-09-327-138C-36
US-09-327-138C-36
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US-09-327-138C-36
US-09-327-138C-36
US-09-327-138C-37
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Maximum Match 100%
Listing first 45 summaries
                                                                                       - nucleic search, using sw model
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Maximum DB seg length: 2000000000
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Match Length DB
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Batent No. 6639063

GREBEAL INFORMATION:
APPLICANT: Unmas Mine Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INTENTION:
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                                                             2.7%; Score 114.2; DB 4;
90.4%; Pred. No. 2.1e-25;
iive 0; Mismatches 13;
US-09-149-476-90
US-08-920-422-17
US-08-921-064-126
US-09-790-988-1
US-08-951-924A-1
US-09-172-339-3
US-09-172-339-3
US-09-245-041-5
US-09-245-041-5
US-09-245-041-5
US-09-589-288-5
US-09-589-288-5
US-09-513-999C-923
US-08-150-331-45
US-08-150-331-45
US-08-150-331-45
US-08-150-331-45
US-08-150-331-45
US-09-270-767-13559
US-09-270-767-13559
US-09-310-185-157
US-09-30-04589-157
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LOCATION: (1).. (1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
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                                                                                             APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ 1D NOS: 23
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.1%; Score 46; DB 4; Length 1141; Best Local Similarity 9.9%; Pred. No. 0.0022; Matches 75; Conservative 280; Mismatches 405; Indels
                                       ; Sequence 22, Application US/09806708B
; Patent No. 6784342
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial sequence
                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: promoter
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                     JS-09-806-708B-22
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Matches 36; Conservative 222; Mismatches 189; Indels
                                                                       MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 APPLICATION DATA: APPLICATION NUMBER: US/08/232,463 PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3%; Score 55.8;
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                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/935,313 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                        ZIP: 22313-0299
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; IMMEDIATE SOURCE: CLONE: pTZgpt-F18 US-08-232-463-14
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       899149
                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 GGTACATTGCTTCTTATTTAGCACTCAC-AGTGGTAGGAATGGGATCCTGGTGCTTCCAC 244
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                                                   2854 GGCAGGCAAAACATTTATACATGTAACGTAATAAATGCATA 2894
                                                                    835 NNNNNNNNAYAWWINKWYYTTDDRWRBAYTNNNNNRWA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: No. 6783969el Nucleic Acids and TITLE OF INVENTION: Polypeptides FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
                                                                                                                                                                    Sequence 875, Application US/09799451
Patent No. 6783969
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Yamazaki, Victoria
Chen, Rui-hong
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Squence o...
General No. 678396>
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
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Zhao, Qing A.
Wang, Jian-Rui
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Best Local Similarity 54.3°
Matches 157; Conservative
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ORGANISM: Homo sapiens
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; LOCATION: (2)
US-09-799-451-875
                                                                                                                                    RESULT 4
US-09-799-451-875
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SEQ ID NO 875
LENGTH: 1063
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3860 TTAAAACATGGCTTGTGTCTTTCCATACACGTCCGGTCAGATTTAAAACTATTTTATAAC 3919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 KRWWWCWARMYRYSTGTRASMWWRRWYYTWMKKWKYAWARAAWRWWAMWWAWRACAAA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 MMRRKYAGKSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWYASKKYMW 307
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1.1%; Score 44.8; DB 4; Length 8
Best Local Similarity 12.0%; Pred. No. 0.004;
Matches 44; Conservative 171; Mismatches 148; Indels
                 Sequence 2813, Application US/09621976
Patent No. 6619063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
PILE REFERENCE: GENSET:054PR2
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APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: 1054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 2813
LENGTH: 832
                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ TWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
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US-09-621-976-2813
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US-09-621-976-2813/c
JS-09-621-976-2813
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-09-007-005-17/c
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APPLICANT: Hong Zhang
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: FTS-0135
CURRENT APPLICATION NUMBER: US/09/657,346A
CURRENT FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 174
SEQ ID NO 96
LENGTH: 30310
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                                                                                                                                                                     2085 TTCTGAGTGGTGTCCTGAGTCTGAAGGAGCTAGCTGCGGGTTCTGGCCACTTCTAGGATCT 2144
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                                                                                                                                                                                                                                                                                                                                                                                                                       2265 ATTICTIGTITATAGICACAAAIAITITAIAGAACAIGAAGGIGIAAAAIAAGITGICTIT 2324
                                                                                                                                                                                               360 WIWWKIWWYWITYIWIRMWWKKKARRWYYWWKSIYACASRYRKYIWGWWWYMWKRMMSI 301
                                                                                                                                                                                                                                                                           300 RWYCYMCWKCCMYRGRRCAWYTWARGRWWSYAWGKWKSGMRSAMSMCTRMYYKKGSTYWTM 241
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                                                                                                                                 Gaps
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Pred. No. 0.76;
0; Mismatches 22; Indels 0;
                                                                                    Query Match
1.0%; Score 42.4; DB 4; Length 832;
Best Local Similarity 12.7%; Pred. No. 0.023;
Matches 43; Conservative 156; Mismatches 137; Indels
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; Sequence 96, Application US/09657346A
; Patent No. 6503754
; GENERAL INFORMATION:
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1.0%;
Best Local Similarity 71.4%;
Matches 55, Conservative 0
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| NAMBYKEY: CDS
| LOCATION: (27235)...(27246)
US-09-657-146A-96
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CDS
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; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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NAME/KEY:
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NAME/KEY:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 TGACAATGTGCGTGTGTTTAAGCTGGGCCTCTTCTCTGGCCTCTGGTGGACTCTGGCTCT
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Patent No. 625858

GENERAL INFORMATION:
APPLICANT: Scottak, Jack W.
APPLICANT: Liu, Richard W.
TITLE OF INVENTION: ENELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: 1903
FILE REFERENCE: 00786/350003
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARRE: PASESEQ for Windows Version 4.0

LENGTH: 289
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APPLICANT: SZORGAK, Jack W.
APPLICANT: SZORGAK, Jack W.
APPLICANT: SZORGAK, Jack W.
APPLICANT: Liu, Richard W.
APPLICANT: Liu, Richard W.
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: PUSIONS
FILE REFERENCE: 00706/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER PLICATION NUMBER: 60/064,491
EARLIER PLICATION NUMBER: 60/064,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.0%; Score 41; DB 3; Length 289; Best Local Similarity 7.6%; Pred. No. 0.026; Matches 17; Conservative 97; Mismatches 111; Indels
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Patent No. 6281344

    LOCATION: (1)...(289)
    OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

TYPE: RNA
ORGANISM: Artificial Sequence
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us-10-017-410-1.rni

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2431 ATTITACTGTAGCTTAAAATATGTTTAAAATGACTTTGAGTGAAATGTTTGTGGCAACCT 2490
                                                        2371 AGICATITGATIGGCGATITTACAAGGCAGGAATACTIGGTITTIGAATGATTGTATATGTC 2430
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                                                                                                         210 TICCAAIAAITIACGCAAIAAAGAITCAICIAGAICAAIAIAITICICITITAIAITITAA 151
     270 AATATCTTGATAATTTATAATTTGATTAATATTTTCAAAATCTATAGTAATTAAAGTCAA 211
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APPLICANT: Gilbert, Mararchn W.
APPLICANT: Wakarchnk, Warren W.
TITLE OF INVENTION: Campylobacter Gilycosyltransferases for Biosynthesis of TITLE OF INVENTION: Gangylosides and Ganglioside Mimics
FILE REPERENCE: 019633-0001100S
CURRENT APPLICATION NUMBER: US 60/118,213
PRIOR PILING DATE: 1999-02-01
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Batentin Ver. 2.1
LENGTH: 1044
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LOCATION: (1)..(1044)
OTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF Sa
OTHER INFORMATION: of LOS biosynthesis locus)
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                                                                                                                                                                                                                                                                  2491 AGGGGTTTATGGATCAGAAT 2510
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09495406; Patent No. 6503744; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   90 AATGGAAAGGATAAGAGAAT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4162 AAAA 4165
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Best Local S
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/248,796A
FILOR PELING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PELING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-02-13
PRIOR PELING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 6940
LENGTH: 435
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; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-248-796A-6940
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                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 41; DB 3; Length 289; Pred. No. 0.026; 97; Mismatches 111; Indels
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SARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Translation template
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; Sequence 6940, Application US/09248796A
; Patent No. 6747137
                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.0%;
Best Local Similarity 7.6%;
                                                                                                                                                                                 ORGANISM: Artificial Sequence
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                                                                                              SEQ ID NO 17
LENGTH: 289
                                                                                                                                                         TYPE: RNA
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gilbert, Michel
APPLICANT: Gilbert, Marchal
APPLICANT: Markerchuk, Warren W.
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019633-00041103
CURRENT APPLICATION NUMBER: US/09/816,028A
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFFWARE: PARCHIN Ver. 2.1
LENGTH: 1044
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Patent No. 6723545
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Gilbert, Michel
APPLICANT: Makarchuk, Warren W.
APPLICANT: National Research Council of Canada
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Campylobacter Glycosyltransferases
FILE REFERENCE: 019633-000111US
CURRENT APPLICATION NUMBER: US/10/303,162
CURRENT FILING DATE: 2002-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3922 CAGGAATTAAACCAAAGCAAATAGAGTACTTTCAGATATAAACTGTGTTTCATACTTTATG
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CTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAc)
CTHER INFORMATION: beta-1,6 N-acetylgalactosaminyl (GalNAc)
CTHER INFORMATION: Liansferase from C. jejuni strain OH4384 (ORF 5a
CTHER INFORMATION: of lipooligosaccharide (LOS) biosynthesis locus)
US-09-816-028A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.0%; Score 40; DB 4; Length 1044; Best Local Similarity 45.7%; Pred. No. 0.16; Matches 139; Conservative 0; Mismatches 165; Indels
RESULT 12
US-09-816-028A-16/c
Sequence 16, Application US/09816028A
Patent No. 6699705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Campylobacter jejuni
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APPLICANT: Gilbert, Michel
APPLICANT: Gilbert, Michel
APPLICANT: Makarchuk, Warren W.
APPLICANT: National Research Council of Canada
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
FILE REFERENCE: 019633-0001100S
CURRENT APPLICATION NUMBER: US/09/495,406
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 1999-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3862 AAAACATGGCTTGTGTCTTTCCATACACATCCGGTCAGATTTAAAACTATTTTATAAACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)...(1044)
CTHER INFORMATION: beta-1,4 N-acetylgalactosaminyl (GalNAC)
OTHER INFORMATION: transferase from C. jejuni strain OH4384 (ORF 5a)
CTHER INFORMATION: of lipooligosaccharide (LOS) blosynthesis locus)
US-10-303-162-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.0%; Score 40; DB 4; Length 1044; 45.7%; Pred. No. 0.16; tive 0; Mismatches 165; Indels
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OTHER INFORMATION: including LOS biosynthesis locus
PRIOR APPLICATION NUMBER: US/09/816,028
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR PILING DATE: 1999-02-01
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 16
LENGTH: 1044
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Patent No. 6503744
GENERAL INFORMATION:
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ORGANISM: Campylobacter jejuni
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Best Local Similarity 45.7
Matches 139; Conservative
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SOFTWARE: Patentin Ver. 2.1
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LENGTH: 11474
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Patent No. 6699705

GENERAL INFORMATION:
APPLICANT: Warren W.
APPLICANT: Wakarchuk, Warren W.
APPLICANT: Omnoral Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
TITLE OF INVENTION: Ganglicside and Ganglicside Mimics
CURRENT APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/118,213
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIN Ver. 2.1
SEQ ID NO 1
LENGTH: 11474
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45.7%; Pred. No. 1.2;
tive 0; Mismatches 165; Indels (
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1.0%; Score 40; DB 4; Length 11474;
Best Local Similarity 45.7%; Pred. No. 1.2;
Matches 139; Conservative 0; Mismatches 165; Indels
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OTHER INFORMATION: including LOS biosynthesis locus
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ORGANISM: Campylobacter jejuni
                                         Query Match
Best Local Similarity 45.73
Matches 139; Conservative
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US-09-816-028A-1/c
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US-09-495-406-1
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11: /cgn2_6/ptodata/2/pubpna/US106_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US106_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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4175
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rıbutıon.			Description	Sequence 1, Appli	Sequence 21, Appl	Sequence 151, App	Sequence 3, Appli	Sequence 6, Appli	Sequence 119, App	Sequence 48, Appl	Sequence 4, Appli	Sequence 2618, Ap	Sequence 2618, Ap	Sequence 611, App	Sequence 50197, A
fived by analysis of the total score distribution. SIMMARIES			ID	US-10-017-410-1	US-10-188-832-21	US-10-295-027-151	US-10-017-410-3	US-10-182-447-6	US-09-917-800A-119	US-09-945-527-48	US-10-182-447-4	US-10-172-118-2618	US-10-342-887-2618	US-10-106-698-611	US-10-242-535A-50197
				13	16	15	13	15							
			Match Length DB	4175	4202	4212	828	822	595	744	792	1098	1098	1473	418
	æ	Query	Match	100.0	17.3	17.3	15.9	15.7	9.6	7.9	4.2	3.1	3.1	9.0	1.6

5019	Sequence 203, Appl Sequence 20, Appl	e 2429,	2069,	109,	129,	34, 7	667,	259,	96	181,	61, 7	287,	601,	16, 1	401,	Sequence 169, App	1, Ag	199	24,	24	1147,	151,	853,	472,	289	5, A	875	150	85	41.	Sequence 63, Appl
US-10-085-783A-50197	US-09-771-208-20	US-10-017-161-	US-10-292-798-20	US-10-322-696-109	US-10	. US-10-311-455-34	US-10-087-192-667	US-09-997-722-259	US-10-367-094-96	US-10-085	US-09-997	US-10-322-281-287	US-10-322-28) US-09-972-546-16	US-10-322	. US-09-997-722-169	US-10-105	US-10-087-192-1999	US-1	US-10-025	US-10-087-1	US-09-997-72	US-10-087-192-853	US-10-221	. US-10-085-117-289	. US-10-182-447-5	; US-10-302-172-875	US-10-311-455-15	US-10-240-589C-8	US-10-322-	US-09-967-768A-63
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9.1		1.4	1.4	1.3	1.3	1.2	1.2	1.2	1.2	1.2	1.1	1.1	1.1	1.1	1.1	1,1	1.1	1.1	1,1	1.1	1.1	1.1	1.1	1.1	1.1	1,1	1.1	1,1	1.1	1,1	1.1
65	61.4	58.2	58.2	55.4	52.6	49.4	49.4	48.6	48.6	48.4	47.6	47.6	47.4	47.4	47	47	47	46.8	46.6	46.6	46.4	46	45.8	45.6	45.6	45.4	45.4	45.2	•	45.2	45
13	0 C	16	17	18	19	20	c 21	c 55	23	N	c 25	7	c 27	c 58	29	30	31	c 32	33	34	c 32	c 36	37	38	c 39	40	41	42	43	C 44	c 45

ALIGNMENTS

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Sequence 1. Application US/10017410
Publication No. US20020115094A1
GENERAL INFORMATION:
APPLICANT: Farnham, Peggy J
APPLICANT: Graveel, Carrie R
TILLE OF INVENTION: Polynucleotide Differentially Expressed in Liver Cancer
TILLE REFERENCE: 960296.97401
CURRENT APPLICATION NUMBER: US/10/017,410
CURRENT FILING DATE: 2001-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CCTGCGGGCTGGCAGTTCGGAGGTGGATTGGTGCGAGGACAACTACACTATCGTGCCTGC 120
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100.0%; Score 4175;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4175; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                             LENGTH: 4175
TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (35)..(859)
US-10-017-410-1
US-10-017-410-1
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                                                         910 GCTGGGCTTCGTTTGCTAGCAAAGATGGCTGAGGGGGTTGAGGAATTGGTGTGGTGTGGG 969
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      17.3%; Score 723.8; DB 15; Length 84.9%; Pred. No. 6e-200; ive 0; Mismatches 142; Indels
                                                                                                                                                                                                                                 Sequence 151, Application US/10295027; Publication No. US20030232350A1; GENERAL INFORMATION:
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Best Local Similarity 84.9
Matches 823; Conservative
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                                                                                                                   970 TGTTTAAAA 978
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                   Length 4202;
                                                                                                                                                                                          Query Match 17.3%; Score 723.8; DB 16; Length Best Local Similarity 84.9%; Pred. No. 6e-200; Matches 823; Conservative 0; Mismatches 142; Indels
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 4202
                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-188-832-21
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                                                                                                                DB 13;
                                                                                                              Score 664.8; DB 13;
Pred. No. 3.8e-183;
0; Mismatches 102;
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Best Local Similarity 87.7%;
Matches 726; Conservative
2.1
                                                                               .. (825)
SOFTWARE: Patentin
SEQ ID NO 3
LENGTH: 828
                                             ORGANISM: Homo
                                                                 ; NAME/KEY: CDS
; LOCATION: (1)
US-10-017-410-3
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              182 GTTCTACAACACGATCAGCAATGTCTTATTTTTTTTTACCGCCCATCTGCATGTGCTT
                                                               GTTTCGTCAGTATGCAACATGCTTCAACAGTGGCATCTACTTAATCTGGACTCTTTTGGT
                                                                                           TGTAGTGGGGATTGGATCTGTCTACTTCCATGCAACGCTGAGTTTCCTGGGTCAGATGCT
                                                                                                        TGTAGTGGGAATTGGATCCGTCTACTTCCATGCAACCCTTAGTTTCTTGGGTCAGATGCT
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Publication No. US20020115094A1
GENERAL INFORMATION:
APPLICANT: Farnham, Peggy J
APPLICANT: Graveel, Carrie R
TITLE OF INVENTION: Polynucleotide Differentially Expressed iFILE REFERENCE: 960296.97401
CURRENT APPLICATION NUMBER: US/10/017,410
CURRENT FILING DATE: 2001-12-14
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                      CAAGGCCCTGTCATCAATTCTGGCCCAGCGAGAAATGGGCCCTTCATTGGTGTCCCCTAT 777
                                                                             CAAGGICCAGICATCAGAITCIGGCCCAGCGAGAAAIGGGCTITITAITGGIGICCCTIAI
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APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Michael
APPLICANT: Castle, Michael
APPLICANT: Castle, Michael
APPLICANT: Gaene Logic, Inc.
TITLE OF INVENTION: MOLECUlar Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR PELICATION NUMBER: US 60/290,029
PRIOR PELICATION NUMBER: US 60/290,645
PRIOR PELING DATE: 2001-05-15
PRIOR PELING DATE: 2001-05-22
PRIOR PELING DATE: 2001-05-22
PRIOR PELING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
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9.6%; Score 400.4; DB 9;
Best Local Similarity 87.9%; Pred. No. 8.3e-106;
Matches 531; Conservative 0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 119, Application US/09917800A
Patent No. US20020119462A1
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SEQ ID NO 119
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Sequence 6, Application US/1018247
Publication No. US20030185814A1
GENERAL INFORMATION:
APPLICANT: HOFMANN, KAY
APPLICANT: RADT, MARCUS
TILLE OF INVENTION: CERAMIDASE
FILE REPERBNCE: P68055U30
CURRENT APPLICATION NUMBER: US/10/182,447
PRIOR PLING DATE: 2002-07-29
PRIOR FILING DATE: 2001-01-27
PRIOR FILING DATE: 2001-01-27
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
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                                                                                                                                             GTATTTACCAAAGATCTTTCGGAATGACAG 399
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APPLICANT: RADT, MATCUS
TITLE OF INVENTION: CERAMIDASE
TITLE REPERENCE: P680055US0
CURRENT APPLICATION NUMBER: US/10/182,447
CURRENT PILING DATE: 2002-07-29
PRIOR PRIJING DATE: 2001-01-27
PRIOR APPLICATION NUMBER: DE 10003293.1
PRIOR FILING DATE: 2000-01-27
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PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 14
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Sequence 48, Application US/09945527
Sequence 48, Application WS/09945527
Publication No. US20030055588A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20030055588A1e1 Nucleic Acid Molecules Encoding
TITLE OF INVENTION: Nucleic Acid and Protein Homologs
TITLE OF INVENTION: Nucleic Acid and Protein Homologs
FILE REFREENCE: 35800/237985
CURRENT APPLICATION NUMBER: US/09/945,527
CURRENT FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 744
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Pred. No. 6.8e-85;
0; Mismatches 38; Indels
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Matches 352; Conservative
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US-09-945-527-48
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Db 532 AAGTCTTGGGCCAGATTCTCAATGGATTTTATAGACATAATTCCCCTGCAAACT 473 Qy 3860 TTAAAAATAATAATTATAACTTTTATAGACTTTTGAATTGTTTCTCTTT 413 Qy 12	RESULT 10 US-10-342-887-2618/c US-10-342-887-2618/c Sequence 2618, Application US/10342887 Publication No. US20040058340A1 GENERAL INFORMATION: APPLICANT: District He, Yudong APPLICANT: Linsley, Peter S. APPLICANT: Mose, Mac APPLICANT: Wan't Veer, Laura Johanna APPLICANT: Van 't Veer, Laura Johanna APPLICANT: Wan de Vijver, Marc J. APPLICANT: Wan de Vijver, Marc J. APPLICANT: Bernards, Rene TILLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients CURRENT APPLICATION NUMBER: US/10/342,887 CURRENT FILING DATE: 2003-01-15 PRIOR FILING DATE: 2003-01-15 PRIOR FILING DATE: 2001-06-18	PRIOR APPLICATION NUMBER: 0.02-05-14
4 AGCGACCAA 4 IGGATATT 4 IGGATATT 5 IGGATATT 6 IGGATATT 6 IGGATATT 7 IGGATATT 7 IGGATATT 7 IGGATATT 8 GCGATATT 6 GCGACTAT 7 IGGATATT 8 GCGACTAT 6 GCGACTAT 6 GCGACTAT 7 IGGATATT 8 GCGACTAT 8 GCGACTAT 8 GCGACTAT 1 IGGATATT 6 GCGACTAT 6 GCGACTAT 7 IGGATATT 8 GCGACTAT 1 IGGATATT 1 IGGATATT 6 GCGACTAT 6 GCGACTAT 6 GCGACTAT 7 IGGATATT 8 GCGACTATT 8 GCGACTAT 1 IGGATATT 1 IG	APPLICANT: Roberts, Chris APPLICANT: Wan 't Veer Laura APPLICANT: Van de Vijver, Marc APPLICANT: Van de Vijver, Marc APPLICANT: Van de Vijver, Marc APPLICANT: Bernards, Rene TITLE OF INVENTION: Dispnosis and Prognosis of Breast Cancer Patients FILE REFERENCE: 9301-175-999 CURRENT APPLICATION NUMBER: US/10/172,118 FRICR FILING DATE: 2002-06-14 FRICR FILING DATE: 2002-05-14 SEQ ID NO 2618 LENGTH: 1098 TYPE: DNA CRGANIGM: Homo sapiens PUBLICATION: INFORMATION: DATABASE ENTRY DATE: 2001-06-18 -10-172-118-2618	3.1%; Score 131.2; DB 15; Length 1098; Best Local Similarity 62.9%; Pred. No. 8.5e-27; Matches 444; Conservative 0; Mismatches 173; Indels 89; Gaps 12; 3527 AAACATGGTTGGAAAATACTGCACCTATTCTATTGGTTGG

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US-10-246.2-250.20197, Application US/10242535A; Sequence 50197, Application No. US20040013663A1
| Publication No. US20040013663A1
| GENERAL INFORMATION:
| APPLICANT: ChondroGene Inc. |
| APPLICANT: Liew, C.C. |
| TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis |
| TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis |
| TITLE OF INVENTION: COMPOSITION NUMBER: US/10/242,535A |
| CURRENT APPLICATION NUMBER: US/10/205. |
| PRIOR APPLICATION NUMBER: US 60/305,783 |
| PRIOR FILING DATE: 2001-02-28 |
| PRIOR FILING DATE: 2001-03-12 |
| PRIOR FILING DATE: 2001-03-12 |
| PRIOR FILING DATE: 2001-03-12 |
| PRIOR FILING DATE: 2001-03-28 |
| NUMBER OF SEQ ID NOS: 59994 |
| SOFTWARE PATENTIN VERSION 3.2 |
| SEQ ID NO 50197 |
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3647 ACCTTCTCTGACTCTCTTCTTCCTCAGGTCTGACAACTAATGGTCTCTGGGGA----- 3700
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US-10-242-535A-50197
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; ORGANISM: Human
US-10-242-535A-50197
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CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT PILING DATE: 2002-03-27
RRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 1090-09-29
PRIOR FILING DATE: 1999-09-29
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8664
SOFTWARE: Patentin Ver. 3.0
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                                                652 TGGATGCTGAAGCTCACCCAGTCAGGGCCCCTCTCCTAGCTCCTTTTACACTGAAATTAA
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; Sequence 611, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 147
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; Sequence 265, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
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; DOCATION: (1)...(77530)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-265
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SOFTWARE: PatentIn version 3.0
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Matches 115, Conservative
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Publication No. US20040037841A1

GENERAL INFORMATION:

APPLICANT: Liew, C.C.

TITLE OF INVERNION: Compositions and Methods Relating to Osteoarthritis

TITLE OF INVERNION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2002

CURRENT FILING DATE: 2002-02-28

FRIOR APPLICATION NUMBER: US 60/305,340

FRIOR APPLICATION NUMBER: US 60/275,017

FRIOR APPLICATION NUMBER: US 60/275,017

FRIOR APPLICATION NUMBER: US 60/275,017

FRIOR FILING DATE: 2001-03-12

FRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

LENGTH: 418
                                                                 AATCITCCCTCACGAGICCTCTTCTCCCAACCCCTACCCAAGCCAACACTGGGATTTGA 3646
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55.4%; Pred. No. 1.1e-07;
Live 0; Mismatches 140; Indels
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Best Local Similarity 55.4%
Matches 201; Conservative
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US-10-085-783A-50197
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; ORGANISM: Human
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Pred. No. 9.2e-06;
0; Mismatches 64; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: NOVel Compositions and Methods in Cancer
FILE REPERENCE: 529452010100.
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 265
LENGTH: 77530
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Fatent No. US20020155564A1
GENERAL INFORMATION:
APPLICANT: BRADFORD, UNAN
APPLICANT: BRADFORD, ERIC
APPLICANT: BRADFORD, ERIC
TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
FILE REFERENCE: 4077-923710US
CURRENT APPLICATION NUMBER: US/09/771,208
CURRENT FILING DATE: 1997-12-29
FRIOR FILING DATE: 1997-12-29
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317888 TTCTGGCCTCTGAGGGCACTGCATACACATGCTGCACAGGTATGCAGAAGAATACCCAC 317829
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Best Local Similarity 60.9%; Pred. No. 0.00017;
Matches 137; Conservative 0; Mismatches 81; Indels 7;
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JOHER INFORMATION: n is unidentified a, c, g, NAME/KEY: misc feature 1.0CATION: (170625)...(170645)
JOTHER INFORMATION: n is unidentified a, c, g, NAME/KEY: misc feature 1.0CATION: (132680)...(132700)
JOTHER INFORMATION: n is unidentified a, c, g, NAME/KEY: misc feature 1.0CATION: (132680)...(132700)
JOTHER INFORMATION: n is unidentified a, c, g, NAME/KEY: misc feature 1.0CATION: (12208-20)
                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (602466)..(602485)
OTHER INFORMATION: n is unidentified a, c, g,
NAME/KEY: misc_feature
LOCATION: (54698)..(547017)
OTHER INFORMATION: n is unidentified a, c, g,
NAME/KEY: misc_feature
LOCATION: (494715)..(494814)
OTHER INFORMATION: n is unidentified a, c, g,
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NAME/KEY: misc_feature
LOCATION: (123459)..(123478)
OTHER INFORMATION: n is unidentified a, c,
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LOCATION: (390986)...(391005)
OTHER INFORMATION: n is unidentified a, c,
NAME/KEY: (346860)...(346823)
OTHER INFORMATION: n is unidentified a, c,
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LOCATION: (280353)..(280373)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (271829)..(271848)
OTHER INFORMATION: n is unidentified a,
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LOCATION: (317174)..(317193)
OTHER INFORMATION: n is unidentified a,
                                                           ORGANISM: Mus musculus
SEQ ID NO 20
LENGTH: 659158
                                        TYPE: DNA
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25		RESULT 1 AK035314 LOCUS AK03 DEFINITION MUS ENELA ACCESSION AK03 VERSI		AUTHORS SAUTHORS STATE OF THE S
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: November 20, 2004, 20:50:47; Search time 11519.4 Seconds (without alignments) 13206.895 Million cell updates/sec Title: Perfect score: US-10-017-410-1 Sequence: 1 ggcacgaggctgctccgataaaaaaaaaaaaaaaa	75 seqs, 18219 satisfying chos	Maximum Match 0% Maximum Match 100% Listing first 45 summaries EST:* 1: gb_est1:* 2: gb_est2:* 3: gb_est2:* 5: gb_est2:* 7: gb_est6:* 6: gb_est6:* 6: gb_est6:* 7: gb_est6:* 8: gb_gss1:* 8: gb_gss1:* 8: gb_gss2:* No. is the number of results predicted by chance to have	Score greater than or equal to the Boore of the result being prand is derived by analysis of the total score distribution. SUMMARIES Query Score Match Length DB ID 3028.8 72.5 3071 3 AK035314 1341 32.1 1341 3 BC023423 780 18.7 10.2 5 BU511164 714.4 17.1 77 7 CN527424 CN537424 U	16.3 688 2 BB108761 BB108761 16.3 688 2 BB108761 BB108761 16.0 670 7 CV721804 CV7218

ACACGTGTGGGGGGTGTGACTAAGACGGGGGCTTGTCACTCGCACCTCTTAGCTTTCCC AGGTTCTCCACGTGTTTGTGGATCCTTCCACTACCTCTGCTGAGAAGGAGGACCACGCCT	362 AGGILLICCANGIGILLIGIGGALCCITCCANLIACCITGCCIGAGAGAGAGAGAGACGACGACGACGACGACGACGACGACG	1485 ATTACATAGACACTATTTCTGCTCTTCCAGAGTGCAGCAGCAGCACCCACAGAGAA 154	1543 TCCTTCAGGTTATGTGAAGATTCCACACAGCCCCCTCTTGTGACCTCTGTGAGAGCAA 1602	1603 GGCCTCG-TTGTAATCGCGGAGGCACTCTGGAGGCTTGACTGTGGAGGCCTGTGAAGA 1661	1662 TITTGGAAAGCTTTCTTAITGGAAGCTTTTGGTGTGTGTGTTACCTCCAAGATTCTGACC 1721 	1722 CCGTTTCTGCTGTTTTTAGGGATATGTGCTTCCTCAGTGACGTACCTCCCTAGGAT 1781	1782 GIGGGCCTCCGGCTTITGTTITCATAATACCTGGTGCTAACTGGTTTCTCAGAGCACTTT 1841 	1842 GCTCTTCTTGATGCTGGGGCGGTCACTACACTCTGATTGGCTGGGGGATCCCAGGGAG 1901	1902 GAAGGGCAGACTCTGACATGAATGTCTCTCACCTGCATCCTACTGTCTTCACTGGGGCTC 1961	1962 TCTTCAGGGTATGAAGTGGGGTATGGGGTATCTCAGGGATGTTTGTAACTCAGGGACCTTC 202		CCGTTCTGAGTGCTCTGAGTCTGAAGGAGCTAGCTGCGGGTTCTGGCACTTCTAGGA	2142 TCTCTTACTCTGTTTAGAACCTTCACAGGTACAAGTGGGAACTGGACTTAAAGAGTTT 2201 	2202 TTAAATGAATAGACTTCATTCTGCTTTTGTGGCTTTTGAGAGTTTTAAAAGTAACTTGCTGG 2261	GCTATTICTIGITIATAGICACAAATATTIATAGAACATGAAGGIGTAAAATAGTTGTC 	2322 ITITATTAAATTCATAGCATTTACCAACTCCCCAGGTAGCAAACACACAC	2382 TGGCGATTTACAAGGCAGGAATACTTGGATTGATGGTATGTAT
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Group Phase I & II Team. TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs JOURNAL Nature 420, 563-573 (2002)		Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,B., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saito,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shihaqawa, A., Shiraki,T.	Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. TITLE Direct Submission	Ā	Kanagawa 230-0045, Japan (E-mail.genome-ree@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216, COMMENT CDNA.library was prepared and sequenced in Mouse Genome	Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to	Prepare Mouse Listures. Please visit our web site for further details. URL:http://genome.gsc.riken.jp/ URL:http://fantom.gsc.riken.jp/.	rce	/ Butania: "C.) but/OUT: /db_xref="FANTOM DB:9530014B21" /db_xref="taxon:10090" /clone="9530014B21" /cov="mails"	/ Lissue type="urinary bladder" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" misc_feature 1	on/ mus 77.	Query Match 72.5%; Score 3028.8; DB 3; Length 3071; Best Local Similarity 99.8%; Pred. No. 0; Matches 3065; Conservative 0; Mismatches 2; Indels 5; Gaps 3;	OY 1065 AGTATCCTTTCCAGGCATACGGCTTGCTGGGTTATGTCCATAATGACATCAACAGAGTA 1124	Qy 1125 GTTCTTTGGGAGACCTAGGGCAACCCAAAGTTTCTTGCTGGAGAGGGTAGCTTGCTGCTTT 1184 Db 62 GTTCTTTGGGACACCTAAGGATTTCTTGCTGGAAGGGTAGCTTGCTGTTT 121	gatgaaag gatgaaag	Qy 1245 GTTCCAGAACTTTTCATTTTGCCGGAGAAAACTGTCCTTCAACAAAACCAAAGTGGGCAAA 1304 Db 182 GTTCCAGAACTTTTCATTTTGCCGGGAGAAACTGTCCTTCAACAAAACCAAAGTGGGCAAA 241	0y 1305 acacgtgtgggggtgtgactaagacgggtggcttgtcactcgcacctcttagctttccc 1364

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 10.2)
National Institutes of Health, Mammalian Gene Collection (MGC)
Mational Institutes of Health, Mammalian Gene Collection (MGC)
Upublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3848
                       TACCCCAGTCACGGGTCAACAGTGTTGTGTTGAGGATCAAACATGGCTCTGTGAAAATAC 3548
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                                                                                                                                                          721 TGCCACCATTCTATTGGTTGGATTCTCAGGAGTCTGAATCTTCCCTCACGAGTCCTCT
                                                                                                                                                                                                                                                                                             CCTCAGGTCTGACAACTAATGGTCTCTGGGGACACCCCAGGTAGGGCCTTCCCCAACTCCT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                    Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 45 Row: C Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                  X., Hulyk, S.W., Hale, S.M., S., Martin, R.G., Muzny, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2829 GGCATTIGGIGCACACGIACATACAGGCAGGCAAAACATTIATACATGTAACGTAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ATACGGATGGATGTGAATGAACATGCTTGGGTGAAAGGAGCCGAGTACCTGACTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 TCTGGTAGAGATGACATCGATGAGTGATGTCGTGACCACTGGGCCCTGCATGGGTGTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3069 ATACGGATGTGAATGAACATGCTTGGGTGAAAGGAGCCGAGTACCTGACTGGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.1%; Score 1341; DB 3; Length 1341; 100.0%; Pred. No. 0; Nismatches 0; Indels 0
                                                                                                                                                                                                                                          This clone has the following problem: frame shifted Location/Qualifiers
                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:5010167"
/tissue_type="Mammary tumor, MM
old mouse. Taken by biopsy."
/clone_lib="NCI CGAP_Mamz"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
              Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 1341; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                           analysis
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/dev stage="embryo." 10.5 dpc"
/lab host="Diper near
/lab host="Diper near
/lab host="Diper near
/lab host="Diper near
/clonellib="NIH BMAP HBAP
/clonellib="Diper Head; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcse
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site .Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not1 and then cloned
directionally into pXX-Asc vector. The library teg
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                CN537424 171 bp mRNA linear EST 29-APR-2004 UL-M-HSO-cgo-o-10-0-UI.rl NIH BMAP_HSO Mus musculus cDNA clone IMAGE:30672249 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                   844 GCCAGTCAAGAT-CACGTGATGGCAAGGCAGTGA--CCAGCTTCTCTATT 900
         Mus musculus (house mouse)
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17.1%; Score 714.4; DB 7; Length 717;
Best Local Similarity 99.7%; Pred. No. 1e-185;
Matches 715; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
strain="C57BL/6"
/db_xref="taxon:10090"
/clone="INAGE:30672249"
/tissue_type="Upper Head"
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Location/Qualifiers
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CN537424.1 GI:46865580
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//mol type="mrNa"
//mol type="mrNa"
//db xref='taxon:10090"
//dome='mrAcE:6505924"
//tissue type="mrndifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 134"
/clone lib="NIH MGC 134"
/clone unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
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   the I.M.A.G.E. Consortium/LLNL at:
found through the I.M.A.G.E. Consorti
http://image.llnl.gov
plate: LiAM14067 row: j column: 05
High quality sequence stop: 681.
Location/Qualifiers
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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bladder"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31]. CDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FIG I."
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Pred. No. 1.6e-176;
0; Mismatches 3;
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/dev_stage="adult"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="9530014B21"
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al Similarity 99.6%;
683; Conservative
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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          61 GGCCCAGCGAGAAAAGGGCTTTTATTGGTGTCCCTTATGTGTCCCTTCTGTGTGCCCACA
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3507

Gaps 0;

them based on alignment. FEATURES Location/Qualifiers location/Qualifiers lorganism="Mus musculus" / mol_type="genomic DNA" / db_xref="taxon:10090" gene <1>61 /locus_tag="HCM1041"	Query Match Best Local Similarity 100.0%; Pred. No. 1.8e-176; Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	OY 182 AIGTGCITCGCCAGIACGCAACGIGCITCAACAGGGCATCTAATAIGGACG 241	Oy 242 CTCCTAGTTGTAGTGGGGATTGGATCTGTCTACTTCCATGCAACGCTGAGTTTCCTGGGT 301	Oy 302 CAGAIGCTIGAAACTIGCCATICTGAGGTTCTGAGGTCTTTGGCCATGTGGTTT 361	QY 362 CCCAGGAGGTATTTACCAAAGATCTTTCGGAATGACAGGGAGGTAGGT	Qy 422 IGIGLOCIGECTGCAALTACAAGGGGTTTATCAAGGCCGCCATCAAGAATATT 481	Qy 482 TCCCTGALGATTCTGGGACTTCCATGGCTGCTTGTTGCAGAGCTGAAGAGTGT 541	Oy 542 GACAAHGEGEHGTGTTTAAGCTGGGCCTCTTCTCTGGCTCTGACTCTGGCTCTC 601	QY 602 TTCTGCTGGATCAGGACCAAGCCTTCTGTGAGCTGCTCTCTTTCACTTCCCCTAC 661 Db 421 TTCTGCTGGATCAGCGACCAAGCCTTCTGTGAGCTGCTTCTTCACTTCCCTAC 480 QY 662 CTGCACTGTGTGGACATATTCTCACTGCTTGCTTCGTTCTTCTTCTTCTTCTTCTTCTTCTTCT
Db 63 CAGTGTTGTGTTGAGGATCAAACATGGCTCTGTGAAAATACTGCCACCCATTCTATTGGT 122 Qy 3568 TGGATTTCTCAGGAGTCTGAATCTTCCCTCACGAGTCCTTTCTCCCAACCCCTACCCG 3627 Db 123 TGGATTTCTCAGGAGTCTGAATCTTCCCTCACGAGTCTCTCTC	OY 3688 TGGTCTCTGGGGACACCCAGCTAGGGCCTTCCCCAACTCCTTATCCAGCTGAACTTGGAT 3747	QY 3748 TCTTCCCAACAGGCTTGACCTGGGTGCTTGGTCCCACTGGCCAACAACACATTT 3807	OY 3808 GGCCAGATTCGGATTCTCAATAGATTTTATAGACATTATTCTCCCACAGACTTTAAAACA 3867	OY 3868 TGGCTTGTGTCTTTCCATACACATCCGTCAGATTTAAAACTATTTTATAACCACAGGAA 3927	OY 3928 TTAAACCAAGCAATAGAGTACTTTCAGATATAAACTGTGTTTCATACTTTTATGTAGAGT 3987	QY 398B GIGCTAIGTAIAGCGGGIAIGIACCTGGCTGAAGIAAITIAACCAIAGCICTGGGAGG 4047	OY 4048 ATTTACAGACCTTTTGCACTTTTTTTTGTGAACTCTGATAACCATGGTCAATATT 4107	Oy 4108 AAAGCCAATAACTGGCATTTTCTGTG 4133	PEFINITION MAY musculus HCM1041 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. ACCESSION AY401891. AY401891. GI:39757877 AY401891. IG:39757877 KEYWORDS GSS. SOURCE Mus musculus (house mouse) Adma, Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Mangé, Z., Zheng, X.H., White, T.J., Sninsky, J.J., Adma, M.D. and Cargill, M. TITLE JUSSER (Lark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wangé, Z., Zheng, X.H., White, T.J., Sninsky, J.J., Adma, M.D. and Cargill, M. TITLE JUSSER (Lark, A.G., Glanowski, S., Mielson, R., Lu, F., Murphy, B., Ferriera, S., Wangé, Z., Zheng, X.H., White, T.J., Sninsky, J.J., Adma, M.D. and Cargill, M. TITLE Juscet Submitted (16-NOY-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA TOMMENT This sequence was made by sequencing genomic exons and ordering

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Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y., Vanderov, A.A., Piao, Y., Matoba, R., Staga, C.A., Bassey, U.C., Wanguren, V., Falco, G., Martin, P.R., Staga, C.A., Bassey, U.C., Wangxar, T.S., Kimber, W.L., Yochikawa, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yochikawa, T., Jaradat, S.A., Pantano, S., Schlessinger, D., Keller, W., Taub, D., Hodes, R.J., Longo, D.L., Schlessinger, D., Keller, J., Klotz, E., Kelsoe, G., Umezawa, A., Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.

Transcriptome analysis of mouse stem cells and early embryos plos Biol. 1 (3), 410-419 (2003)

Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
Mational Institute on Aging/National Institutes of Health
                                                                                                                        956 AGGICTICACCACTAACGGICTICTICGGGACACCTAACTAGGGCCTCCCCCAGCTCCTTCCT 1015
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(Long) Mus
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Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 670)
                                                                                                                                                                                                            CCGCCTCCCAGATC - - CACTGGGATTTGAACCTTCAAATCCTGCCTCTCTTCTTCTTCTTTC
                                                                            AGGTCTGACAACTAATGGTCTCTGGGGACACCCAGCTAGGGCCTTCCCCAACTCCTT-AT
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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Plate: E0830 row: A column: 03
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                                                                                      Shultz, M.A., Zhang, L., Gu, Y.-Z., Baker, G.L., Fannuchi, M.V., Padua. A.M., Gurske, M.A., Morin, D., Penn, S.G., Jovanovich, S.B., Plopper, C.G. and Buckpitt, A.R. Gene expression analysis in response to lung toxicants: I. Gene expression analysis in response to lung toxicants: I. Sequencing and microarray development A.M. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
Contact: Shultz M. Galifornia, Davis
University of California, Davis
University of California, Davis
1311 Haring Hall. One Shields Avenue, Davis, CA 95616, USA Tel: S30 752 4698
Email: mashultz@ucdavis.edu
Average Phred score is 20 or better. All poor quality data (Phred < 20) and vector/linker sequence has been removed.
High quality sequence stop: 1388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="airway or parenchyma"
/dev stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/note="Organ: lung; Vector: pGEM-11Zf(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung_airways and parenchyma tissues."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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16.1%; Score 670.6; DB 6;
Best Local Similarity 87.2%; Pred. No. 1.7e-173;
Matches 854; Conservative 0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="mRNA"
/strafn="Sprague-Dawley"
/db_xref="taxon:1016"
/clone="Contig3708"
                                                                            (bases 1 to 1388)
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                              AK085306 1173 bp mRNA linear HTC 03-APR-2004 Mus musculus 0 day neonate Kidney CDNA, RIKEN full-length enriched library, clone.D630008PO7 product:similar to CANCER RELATED GENE-LIVER 1 [Mus musculus], full insert sequence.
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2750 AGACGACCCAGCGACTIGIGAGGCTCATAACCAGCAACTCCAGCCCTGGGGCATCTGACG 2809
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6 (bases 1 to 1173)
Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
                             Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                               RIKEN Genome Exploration Research Group Phase II Team and
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.8ng of mRNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The CDNAs were ligated to Lone-linker LL-Sad4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and Not1 enzymes and cloned into Sal1/Not1 site of pCMV-SPORT6 plasmid vector. The DHIOB E. coll host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2Kb. The library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2449
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                                                                                                                                                                                                                       /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sall;
Site_2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Rese 11: 1553-1558 (2001). [PMID: 11544199]). The
mRNAS were extracted from a pool of 360 embryos at 4-cell
stage. Double-stranded cDNAS were synthesized with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300
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                                                                                                                                               /clone_lib="NIA_Mouse four-cell-Embryo cDNA library (Long)"
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/db_xref="niaEST:E0830A03-5"
/db_xref="taxon:10090"
/clone="NIA:E0830A03 IMAGE:30908450"
/tissue_type="4-cell stage embryo"
/dev stage="4-cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.0%; Score 668.4; DB 7; ilarity 99.9%; Pred. No. 5.5e-173; Conservative 0; Mismatches 1;
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Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus

Butaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

B 1 (bases 1 to 955)

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Hara,A., Hiramoto,K., Hori,F., Ishi,Y., Ito,M., Kawai,J.,

Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,

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RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
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AV227941 RIKEN full-length enriched, 14 days embryo liver Mus musculus cDNA clone 4432411104 3', mRNA sequence.
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Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome_resegrac.riken.jp, URL:http://genome.gsc.riken.jp/
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Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GCGTGTGTTTAAGCTGGCCTCTTCTCTGGCCTCTGGTGGACTCTGGCTCTTTTTTCTGTG
                                                                                      GTATTTACCAAAGATCTTTCGGAATGACAGGGGCAGGTTCAAGGCAGTGGTGTGTCTCT
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db_xref="G1:26551559"
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LLVABLKRCDNVRVFKLGLFSGLMWTLALFCWISDQAFCELLSSFHFPYLHCVWSADR
G"
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramateu, M. and Hayashizaki, Y.

Direct Submission

Bubmitted (IG-ARP-2002) Yoshihide Hayashizaki, The Institute of Submitted (IG-ARP-2002) Yoshihide Hayashizaki, The Institute of Brypical and Chemical Research (RIKEN), Laboratory for Genome Bryloration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, I-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, URL: http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
Strain="167BL/6J"

/db_xref="FANTOM_DB:D630008P07"

/db_xref="raxon:10090"

/clone="D630008P07"

/tissue type="kidney"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dov stage="0 day neonate"
                                                                                                                                                                                                                                                                                                                                                 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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similar to CANCER RELATED GENE-LIVER 1 [Mus musculus]
(SPTR|AAL40408, evidence: FASTY, 100%ID, 77.8%length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTCTACAACACGATCAGCAACGTCTTTTTTTTTTTTTACCTCCCATCTGCATGTGCTT
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
1.cation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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/note="Organ: mammary; Vector: pcWV-SPORT6; Site 1: SalI;
/note="Organ: mammary; Vector: pcWV-SPORT6; Site 1: SalI;
site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Glibert Smith, NIH"
                                                                                                        TGTGTCTTTCCATACACATCCGGTCAGATTTAAAACTATTTTATAACCACAGGAATTAAA
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                                           GATTGGGATTCTCAATAGATTTTATAGACATTATTCTCCCCACAGACTTTAAAAACATGGCT
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Plate: LiAM13955 row: g column: 14
High quality sequence stop: 679.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="timor, blopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
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/clone="IMAGE:6437893"
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/strain="FVB/N-3"
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                                                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNCTCGGGAAATGGTGTCNACACA-GGAAAAGTGCCTACCCCAGTCACGGGTCAACAGTG 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Site 1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
nonredundant cDNA library. Genome Res. . 11 (2), 281–289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I.,
Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
Hayashizaki,Y.
                                                                                                      Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="RIKEN full-length enriched, 14 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3633 ACACTGGGATTTGAACCTTCTCTGACTCTTCTTCCCTCAGGTCTGACAACTAATGGTC
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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/clone="4432411104"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="liver"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                     prepare mouse tissues.
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617 bp mRNA linear EST 29-APR-2002 UI-M-CGOp-bfj-a-09-0-UI.rl NIH_BMAP_Ret4_S2 Mus musculus cDNA clone UI-M-CGOp-bfj-a-09-0-UI 5', mRNA sequence.
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SAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1065 AGTATCCTTTCCAGGCATACGGGCTTGCTGGGTTATGTCCATAATGACATCAACAGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 ACACGIGIGGGGGGIGIGACIAAGACGGGIGGCTIGICACICGCACCICTIAGCITITCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1365 AGGTTCTCCACGTGTTTGTGGATCCTTCCACTACCTCTGCTGAGAGATGGAGCCACGGCT
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al Similarity 98.8%;
641; Conservative
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ALIA MAYASHILZARI, 1.

ALIA MAYASHILZARI, 1.

BEQUENCING Pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                          BB627599 RIKEN full-length enriched, adult male urinary bladder Musmussulus cDNA clone 9530014B21 5', mRNA sequence.
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                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 651)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Marsuyama, T., Miyazaki, A., Nomura, K., Sano, H., Sasaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takem Muuse ESTS (Kakawa, T., Muramatsu, M. and Hayashizaki, Y. Unpublished (2001)
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RIKEN. Division of Experimental Animal Research in Riken
Contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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/dev_stage="adult"
/lab_host="DH108"
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/db_xref="taxon:10090"
/clone="9530014B21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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   1 (bases 1 to 617)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: Dr. Xin-Yuan Fu, Yale University School of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Gaps
                                                                                                                                                                                                                                                                    Contact: Chin, H
Mational Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
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                                                                                                                                        Genome Res. 6 (9), 791-806 (1996)
97044477
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
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                                                                                                                        discovery
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS 03-OCT-2000
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                                   TGTAACTCAGGCACCTTCTGCTTTCTGACATTCCATTGTCAGTGAGACTGCACTCCAG 479
                                                                                                                                                                                                                                                      540 GTTCTGGCA-TTCTAGGATCTCTTACTCTGTTTAGAACCTTCACAGGGTACAAAGTGGGA 598
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Rose, M., Muright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ411514 606 bp DNA linear GSS 03-OCT-200
1M0184B07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Genome Center
Rm. 308 Blomedical Polymers Research Bldg., 20 S. 2030 B., SLC,
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus G57BL/60 (male) was obtained from the Jackson
                                                                                                                clone UUGCIM0184B07 R, genomic survey sequence.
AZ411514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@qenetics.utah.edu
Insert Length: 10000 Std Error; C
Plate: 0184 row: B column: 07
Seq primer: CACACAGGAAACAGCTATGACC
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/mol_type="genomic DNA"
/strain="CS7BL/6J"
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Location/Qualifiers
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/clone="UUGC1M0184B07"
                                                                                                                                                                                                                                                                                                                                            2184 ACTGGACTTAAAGAGTTTT 2202
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Mus musculus
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KEYWORDS
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us-10-017-410-1.rst

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of pWD42 (gi|4732114|gp|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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ORIGIN

1185 1425 1543 1604 GCCTCGTTGTAATCGCGGAGGCAGCTTGAGCTTGAGTGGAGCGCCTGTGAAGATT 1663 1066 GTATCCTTTCCAGGCATACGGCTTGCTGGGTTATGTCCATAATGACATCAACAGAGTAG 1125 CACCATTTCCAGACTCTCAACCCCTGATAAACAAGACCTTCTGATTTGGTGATGAAAGG 1245 TICCAGAACTITICATITITGCCGGGAGAAACTGTCCTTCAACAAAACCAAGTGGGCAAAA 1305 CACGIGIGGGGGGGGGTGACTAAGACGGGTGGCTIGTCACTCGCACCTCTTAGCTTICCCA 1365 CAGAGGGCAAAGCTGGCAACACCCTCTATGCCAAAAGCTACACTCCTTTAAGCACACA 1485 7 547 487 367 247 187 CCTTCAGGTTATGTGAAGATTCCACACACACCCCCTCTTGTGACCTCTGTGAGAGCAAG 1603 307 THACATATAGACACTATTTCTGCTCTTCCAGAGTGCAGCAGCCTCAGAGCCACAGAGAAT 127 427 67 8 GTATCCTTTCCAGGCATACGGGCTTGCTGGGTTATGTCCATAATGACATCAACAGAGTAG TTCTTTGGGAGCACCTAGGGCAACCCAAAGTTTCTTGCTGGAGAGGGTAGCTTGCTGTTTC CACCATTTCCAGACTCTCAACCCCCTGATAAACAAGACCTTCTGATTTGGTGATGAAAGG TTCCAGAACTTTTCATTTTGCCGGGGGGAGAAACTGTCCTTCAACAAAACCAAGTGGGCAAAA CACGTGTGGGGGGTGTGACTAAAACGGGGGGGCTTGTCACTCGCACTCTTAGCTTTCCCA CAGAGGCCAAAGCTGCCAACACCCTCTATGCCAAAAGCTACACTCCTTTTAAGCACACA TTAC--ATAGACACTATTTCTGCTCTTCCAGAGTGCAGCAGCCTCAGACCCACAGAGAAT GCCTCGTTGTAATCGCGGAGGCAGCTCTGGAGGCTTGACTGTGGAGGC-CTGTGAAGATT 306 GGTTCTCCACGTGTTTGTGGATCCTTCCACTACCTCTGCTGAGAGATGGAGCCCACGGCTT 3; Gaps Query Match
13.8%; Score 576.8; DB 8; Length 606;
Best Local Similarity 99.2%; Pred. No. 1.2e-147;
Matches 601; Conservative 0; Mismatches 2; Indels 3 909 1126 546 1186 486 1246 426 1306 366 1366 1426 246 1486 186 1544 126 99 g à Q ð g 8 8 à a QY Db ò d ò Q à Ω ð

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CQ736906 Sequence
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CQ605547 Sequence
BX005084 Mouse DNA
BX324222 Mus muscu
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Mus musculus cancer related gene-liver 1 mRNA, complete cds.
AF282864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases I to 4174)
Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Expression profilling and identification of novel genes in hepatocellular cardinomas
                                                                                 Sequence
Homo sapi
Sequence
                   BC059819 Mus muscu
                                 Ciona int
Drosophil
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Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Garcinomas using oligonucleotide microarrays and representational difference analysis
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Farnham, P.J. and Graveel, C.R.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. IMO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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Submitted (09-JAN-2002)
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                                                                                                                                 Patent: WO 0155408-A 6 02-AUG-2001;
Memorec Medical Molecular Research Cologne Stoffel GmbH (DE)
Location/Qualifiers
                                                                    Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                      822
246
115
113
                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                        /organism="Homo mapienm"
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/db_xref="taxon:9606"
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                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Hofmann, K. and Conradt, M.
              GI:15394643
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1373.50
94.91%
                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                              89.45%
90.84%
                                                      Homo sapiens
 AX206799
AX206799.1
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DNA linear PRI 09-JAN-2002
from 2, complete sequence.
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Submitted (09-DBC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 149462)
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                                                                                                                                            GinGlyProValileArgPheTrpProSerGluLysTrpAlaPheIleGlyValProTyr 260
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all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats, all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                              CAAGGCCCTGTCATCAAATTCTGGCCCAGCGAGAAATGGGCCCTTCATTGGTGTCCCCTAT 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGlu
                                    GCTGCCTACCTGGGCTGTGTATGCTTTGCCTACTTTGATGCTGCCTCAGAGATTCCTGAG
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                                                                                                                                                                                                                                                                                                                             778 GTGTCCCTCCTGTGTGCCAACAAGAAATCATCAGTCAAGACCACG 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of Homo sapiens BAC clone RP11-470J24
Unpublished (2001)
3 (bases 1 to 149462)
                                                                                                                                                                                                                                                                                 ValSerLeuLeuCysAlaHisLysLysSerProValLysIleThr
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Contact: sapiens@watson.wustl.edu
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Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nguyen, C., Doebber, A. and Kozlowicz, A.
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Homo sapiens BAC clone RP11-470J24
AC017081
AC017081.8 GI:18093316
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Sulston, J.E. and Waterston, R.
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Louis

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Length:
Matches:
Conservative:
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10758...11039
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9685. .9973
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8000. .8436
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8437. .8540
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18177. 18501
/rpt family="L1"
/rev. 1819. 2010
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10280. .10305
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12966. .13140
/rpt family="L1"
13139. .16061
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11999. .12591
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2707. .12952
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20490. 20906
/rpt_family="L1"
21258. 21365
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2592. .12706
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_family="L1"
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                                                                                 'rpt_family="L2"
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1361.50
94.91%
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Pred. No.:
          The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The clone sequenced to the left is RP11-310K15, 2000 bp overlap, the clone sequenced to the right is RP11-156A1, 2000 bp overlap. Actual start of this clone is at base position 190775 of RP11-310K15; actual end is at base position 28935 of RP11-156A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .771. .2127
'note="match to EST AW614820 (NID:g7320006) hg80c08.xl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="match to EST AA056210 (NID:g1548612) zf62g06.s1"
                                                                                                                                                                                                                                   The sequence between 81601 and 81703 is covered only by a pcr product of clone DNA. Unresolved tandem repeat regions exist between 81548 and 83183, 126196 and 127426.

Location/Qualifiers
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486. .3527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6153. .6244
/rpt_family="MER1_type"
6965. .7000
/rpt_family="AT_rich"
7020. .7094
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/db_xref="taxon:9606"
/chromosome="2"
                                                                                                                                   VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
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4231. .4273
/rpt_family="AT_rich"
5518. .5848.
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808. .6116
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141. 282
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501. 270
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65._.1037
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802
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153_ ,624
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991___3224
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                                                                                                                                                                                                                                                                                                   source
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us-10-017-410-2.rge

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 4078)
Straubsberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klauener, R.D., Colling, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, F., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullek, J.A., Gunaratne, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Hale, S., Garcia, A.M., Madan, A., Young, A.C., Shevchenko, Y., Bukfesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 132 Row: o Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314857.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Stavanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Ietticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Dannes Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapber@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
DNA Sequencing Dy: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/product="CRG-L1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Brain"
/clone_lib="NIH_BMAP_GH0"
/lab_host="DH10B"
/note="Vector: pYX-ASC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="LocusID:230379"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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AUTHORS
TITLE
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PUBMED
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                                        REFERENCE
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COMMENT
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                                                                                                                                                                                                 136861 GAGGACAACTACACCATCGTGCCTGTTGCGGGGGTTCTATAACATGATCAGCAATGTC 136802
                                                                                                                                                                                                                                                                                                                                                                                                                             136801 TTATTTTTTTTTTACCGCCATCTGCATGTGCTTTTTTCGTCAGTATGCAACATGCTTC 136742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136683 TTCCATGCAACCCTTAGTTTCCTGGGTCAGATGCTTGAAGATTGCAGTCCTTTGAGGTT 136624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136503 TTTGTCAAGCCTGCCATCAACATCTCTCTGATGACCCTGGGGAGTTCCTTGCGCTGCA 136444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136623 Crdargrargracarcargracarccccagaaggrarcraccaaagarcrrrcgaaar 136564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136563 GACCAGGGTAGGTTCAAGGTGGTCTGTGTCTGTCTGTCAGATTATGACGTGCCTGGCA 136504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136443 CTGCTCATCACAGAGCTAAAGAGGTGTGACAACATGCGTGTTTTAAGCTGGGCCTCTTC 136384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AspArgGlyArgPheLysAlaValValCysValLeuSerAlaIleThrThrCysLeuAla 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuMetCysAlaLeuAlaMetTrpPheProArgArgTyrLeuProLysIlePheArgAsn 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PhellelysProAlalleAsnAsnIleSerLeuMetIleLeuGlyLeuProCysThrAla 160
                                                                                                                                                                                                                                                                                                                                                                              09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                   1 MetGlyAlaProHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys 20
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136323 CTGCTGTCGTTCCAACTTCCCCTACCTGCATGCATGTGGCACATCCTCATCTGCCTT
                                                                                                                                                                                                                                                                                                                                                                            LeuPhePheIleLeuProProIleCysMetCysLeuPheArgGlnTyrAlaThrCysPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AsnSerGly11eTyrLeu11eTrpThrLeuLeuValValValGly11eGlySerValTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuLeuSerSerPheHisPheProTyrLeuHisCysValTrpHisIleLeuIleCysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 AlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GlnGlyProVallleArgPheTrpProSerGluLysTrpAlaPheIleGlyValProTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheHisAlaThrLeuSerPheLeuGlyGlnMetLeuAspGluLeuAlaIleLeuTrpVal
                                                                                                                                                                                                                                                                       GluAspAsnTyrThrIleValProAlaIleAlaGluPheTyrAsnThrIleSerAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC059819 4078 bp mRNA linear ROD 21-
Mus musculus cancer related gene-liver 1, mRNA (cDNA clone
MGC:69583 IMAGE:6839525), complete cds.
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             140
             Mismatches:
Indels:
                                                                                                               US-10-017-410-2 (1-275) x AC017081 (1-149462)
                                                              Gaps:
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             Best Local Similarity:
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                                        Query Match:
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KEYWORDS
SOURCE
ORGANISM
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BC059819
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linear INV 30-NOV-2002 full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MetTrpPheProArgArgTyrLeuProLysIlePheArgAsnAspArgGlyArgPheLys 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 ACTIGGCTACCAAAGGAAATATCTCCCTTCGATTCTCAGATCAGACAGGCGAAATTTTCCAA 454
                                                                                                                                                                                        Urochordata; Ascidiacea; Enterogona;
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-OCT-2002) Nori Satoh, Kyoto University, Department
Zoology; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
(E-mail:satoh@ascidian.zool.kyoto-u.ac.jp, Tel:81-75-753-4095,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TrpAspHisLeuArgAlaGlySerSerGluValAspTrpCysGluAspAsnTyrThrIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 ValProAlaileAlaGluPheTyrAsnThrIleSerAsnValLeuPhePheIleLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 ProlleCysMetCysLeuPheArgGlnTyrAlaThrCysPheAsnSerGlyIleTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 IleTrpThrieuLeuValValValGlyIleGlySerValTyrPheHisAlaThrLeuSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheLeuGlyGlnMetLeuAspGluLeuAlaIleLeuTrpValLeuMetCysAlaLeuAla
                                                                                                                                                                                                                       Satou,Y., Yamada,L., Mochizuki,Y., Takatori,N., Kawashima,T. Sasaki,A., Hamaguchi,M., Awazu,S., Yagi,K., Sasakura,Y., Nakayama,A., Ishikawa,H., Inaba,K. and Satoh,N. A cDNA resource from the basal chordate Ciona intestinalis Genesis 33 (4), 153-154 (2002)
 GIGLOCCTICTGTGTGTCCCACAAGAAGTCGCCCAGTCAAGATCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1429
135
52
74
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ghost.zool.kyoto-u.ac.jp/indexrl.html).
Location/Qualifiers
1. 1429
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_txef="taxon:7719"
/clone="citbol3n14"
                                                                            1429 bp mRNA clone:citb013n14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                            AK116177 1429 bp Ciona intestinalis CDNA, clone:cith AK116177 AK116177. GI:23588622 FLI CDNA. Ciona intestinalis Ciona intestinalis Ciona intestinalis Eukaryota; Metazoa; Chordata; Urocl Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax:81-75-705-1113)
Ciona intestinalis cDNA Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1-1429)
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                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1429)
Satou, Y. and Satoh, N.
Direct Submission
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NTFSNFLFILLPPVLIMLFKEYGRFVTPGIHVIWVLLIVVGLSSMYFHATLSLIGQLL
DELAILWVFWAAFGLFYPKRYYPKFWKNDRKTFSWLMLLSAIAATGLSWWKPIVNAFV
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Conservative:
Mismatches:
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/db_xref="FLYBASE.FBgn032842"
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/db_xref="taxon:7227"
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/note="Longest ORF"
       cdna@fruitfly.berkeley.edu.
                                                                                                                                                                    /map="38B4-38B5"
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Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection | (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polya tail and contiguity
within 100 Kb in the genome. Thus we believe the Sequence to
reflect accurately this particular cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcription of unspliced precursor RNAs, and
reverse transcription about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
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Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Beyaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Bphydroidea; Drosophilide; Drosophila.

1 (bases 1 to 2318)

Stapleton,M., Broketein,P., Hong,L., Agbayani,A., Carlson,J.,

George,R., Gnzalez,M., Gusrett,V., Dresnek,D., Farfan,D., Frise,E.,

Miranda,A., Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S.,

Patel,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Rubin,G.M.
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                          AsnAsnIleSerLeuMetIleLeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeu 166
                                                                                                                                                                                   LysArgCysAspAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTrpTrr 186
                                                                                                                                                                                                               LeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHis 206
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                                                                                                                     AY071232 2318 bp mRNA linear Drosophila melanogaster RE26924 full length cDNA.
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FIL CDNA.
Drosophila melanogaster (fruit fly)
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                 303 TCATCCAACATCGCCGAGTTCGTGAACACGTTTAGCAACTTCCTGTTCATCCTACTGCCG 362
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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27 ValProAlaIleAlaGluPheTyrAsnThrIleSerAsnValLeuPhePheIleLeuPro
                                                               ProlleCysMetCysLeuPheArgGlnTyrAlaThrCysPheAsnSerGlylleTyrLeu
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Patent: WO 0155408-A 4 02-AUG-2001;
Memorec Medical Molecular Research Cologne Stoffel
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/db_xref="taxon:9606"
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Sequence 4 from Patent WO0155408.
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NTFSNFLFILLPPYLIMLFKEYGRFYTPGIHYIWVLLIVVGLSSMYFHATLGLIGQLL
DELALLWVFMAAFSLFYFKRYYPKFVKNDRKTFSWLMLLSALAATGLSWKPIVNAFY
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KALRNTI"
                                                                  1051
                                                                                                                               1052 TTTCCATACCTGCACGCTTCTGGCACATATTCATTTTTATAGCCGCCTACACGGTGCTG 1111
                                                                                                                                                                                      1112 GTGCTTTTCGCCTACTTCTACGTGGAATCGGAGCTGCCCCAGCGACAGCCGCTGCTGAAG 1171
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Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Merazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilae; Drosophila.
Ephydroidea; Drosophilae; Drosophila.
Disect Submission.
Direct Submission
Submitted (24-NOV-2000) Institut de Neurobiologie Alfred Fessar Avenue de la Terrasse. Bat 32/33, Gif-sur-Yvette 91190, France
Location/Qualifiers
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                                                    CAGAGAGTTAGTGACCAGAGGGTCTACCGCCTGGGCATCCGATCGACGACGGTCTGGGCT
                                 LeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHis
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|mol_type="mRNA"
| db_xref="taxon:7227"
|chromosome="2"
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/product="brain washing"
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/gene="bwa"
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Mao,C., Xu,R. and Obeid,L.M.
Direct Submission
Submitted (08-FEB-2001) Medicine, Medical University of Carolina, 171 Ashley Avenue, Charleston, SC 29425, USA
1. 795
   Molecular cloning and
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2 (bases 1 to 795)
                  ceramidase
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102
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            Conservative:
Mismatches:
   Matches:
                                      Indels:
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                                                                        US-10-017-410-2 (1-275) x AX206797
549.50
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       Percent Similarity:
Best Local Similarity:
Query Match:
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/translation="MOSIFAYQSBUDMCBSNFQYSBLVABFYNTFSNIPFFIFGPLM MLMHPYAQRRSRYTYVWWLEMITGLFSWYFHMTLSFLGQLLDBIALLWLLGSGYSI WRDKVFFSBELGGNRSQFIRVFITYVVXTLLGFRPTVATALNSIALHILYIVCQB YRKTSNFELBHLIBYSVVLAMALTSWISDRLLCSFWQRIHFFYLHSIWHVLISITFP YGMVTMALVDANYEMBGETLKVRYWPRDSWPVGLPYVBIRGDDKDC"

sphingosine

to generate

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a fatty acid"
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69 GCTGGTGGCCGAGTTCTACAACACGTTCTCCAATATCCCCTTCTTCATCTTCGGGCCACT 128
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Conservative:
Mismatches:
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PRI 02-MAR-2002

Ar34/U24 1962 1965 bp mRNA linear Homo sapiens alkaline ceramidase mRNA, complete cds. AF347024

AF347024.1 GI:19070366 Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

Homo sapiens

AUTHORS REFERENCE

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 795)
Mao,C., Xu,R. and Obeid,L.M.

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03-FEB-2004
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                                                                                                                                                                                            Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Matches:
Conservative:
Mismatches:
Indels:
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PE Corporation (NY) (US)
Location/Qualifiers
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Sequence 22840 from Patent W002068579.
CQ736906.1 GI:42333767
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Sequence 22839 from Patent WO02068579.
CQ736905
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                       208 ofyrieuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCy
                                                                     609 CTATCTGCACAGCATCTGGCATGTGCTCATCAGCATCACCTTCCCTTATGGCATGACC
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                                                                                                           228 sPheAlaTyrPheAspAlaAlaSerGluIleProGluGlnGlyProValIleArgPheTr
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Mismatches:
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                                                                                                                                                                                                                                              315 bp DNA
Sequence 30030 from Patent W002068579.
CQ744096
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Mao.C., Xu,R., Szulc,Z.M., Bielawski,J., Becker,K.P., Bielawska,A., Galadari,S.H., Hu,W. and Obeid,L.M.
Cloning and Characterization of a Mouse Endoplasmic Reticulum Alkaline Ceramidase: AN ENZYME THAT PREFERENTIALLY REGULATES
METAHOLISM OF VERY LONG CHAIN CERAMIDES
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Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Molecular cloning and characterization of a novel murine alkaline
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Mismatches:
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PE Corporation (NY) (US)
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Mao,C., Xu,R. and Obeid,L.M.
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Direct Submission
Submitted (08-FBB-2001) Medicine, Medical University of
Carolina, 171 Ashley Avenue, Charleston, SC 29425, USA
Location/Qualifiers
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Abv22064 Human pro
Ab190053 Human pol
Aaf13013 Aspergill
Aaf13013 Aspergill
Aah07955 Human CDN
AdA67192 Human GDN
AdA67192 Human GPC
Aav21511 Staphyloc
Ab123205 Drosophil
Ab123205 Drosophil
Ab123205 Drosophil
Ad687290 Human GPC
Aa880960 DNA encod
Aa66668 DNA encod
Aa66689 Human tum
Aad58279 Human tum
Adl06642 Human 3T3
Adi21948 Novel hum
Adi21468 Novel hum
                                                                                                                                                                                                                                                                                                              Abz52533 Aspergill
Adc87292 Human GPC
Adj12462 DNA fragm
                                                                                                                                                                                                                                                                                            Adc87619 Human GPC
Adc86916 Human GPC
                         Aak51566 Human pol
Aak52550 Human pol
Aah48639 Human cer
                                          Aah48639 H
Ab124043 D
Ab124042 D
Ab130432 D
Aah48640 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Liver tumour marker protein, CRG-L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse cDNA encoding a liver tumour marker protein, CRG-L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; ss; gene; liver cancer; liver tumour; CRG-L1; hepatocellular cancer.
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ADC87290
AAS80960
AAS66068
AAD58280
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ADC87616
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ADC87192
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ABL24043
ABL24042
ABL30432
AAH48640
ABZ11993
ADM44511
AAA96499
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ABV22202
ABV22064
ABL90053
AAS79600
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AAH07955
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35. .862
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  JS2002115094-A1
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Acc50961 Human bla
Adn38833 Cancer/an
Abs54149 Human cDN
Aah48641 Human cer
Ad106640 Human 3T3
                                                                     (without alignments)
3333.928 Million cell updates/sec
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                                                                                             US-10-017-410-2
1512
1 MGAPHWMDHLRAGSSEVDWC......IGVPYVSLLCAHKKSPVKIT 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                             November 20, 2004, 21:28:52; Search time 433 Seconds
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                            nucleic search, using frame plus p2n model
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                                                                                                                                                                                 4134886 segs, 2624710521 residues
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Searched:

Title: Perfect score:

Sequence:

OM protein

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Scoring table:

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The invention relates to a polypeptide designated as CRG-L11), which is differentially expressed in liver tumours relative to normal expression in normal liver tissues, designated CRG-L1. Also included are the encoding polynucleotides (in the case of the human sequence, mapping to chromosome 9p), expression constructs, host cells, anti-CRG-L1 antibodies, identifying modulators of CRG-L1, and the use of the CRG-L1 sequence in the diagnosis of hepstocallular cancer in tumour cells from a liver of a human or non-human animal. The CRG-L1 protein and polynucleotide are useful as diagnostic markers for a liver cancer in humans animals, and as a system for assessing putative
                                                                                                       Novel polypeptide designated as CRG-L1, useful as diagnostic marker for liver cancer, is differentially expressed in liver tumors relative to normal liver tissues.
                                                                                                                                                                                                                                                                                                                                                                                                  therapeutic agents. The present sequence encodes mouse CRG-LI
                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 962 A; 971 C; 1012 G; 1230 T; 0 U; 0 Other;
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10-017-410-2	-2 (1-275) x ABS54148 (1-4175)
35	MetGlyAlaProHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys 20
21	GluAspAsnTyrThrIleValProAlaIleAlaGluPheTyrAsnThrIleSerAsnVal 40
41	LeuPhePhelleLeuProBrolleCysMetCysLeuPheArgGlnTyrAlaThrCysPhe 60
61 215	AsnSergly1leTyrLeu1leTrpThrLeuLeuValValValGly1leGlySerValTyr 80
81 275	PheHisAlaThrLeuSerPheLeuGlyGlnWetLeuAspGluLeuAlaIleLeuTrpVal 100
101	Leumet Cysalaleualamet TrpPheProargargTyrLeuProlys11ePheArgasn 120
121 395	ABPArgGlyArgPheLysAlaValValCysValLeuSerAlaileThrThrCysLeuAla 140
141	PhelleLysProAlaIleAsnAsnIleSerLeuMetIleLeuGlyLeuProCysThrAla 160
161	LeuleuvalaladluleulysargcysaspasnvalargvalPhelysleuGlyleuPhe 180
181	SerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGlu 200

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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a blological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 encode the human bladder cancer-associated proteins given in ABR48146 to ABR48342). Bladder cancer-associated proteins given in ABR48146 to ABR48342). Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
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                       TCTGGCCTCTGGTGGACTCTGGTCTCTTCTGCTGGATCAGCGACCAAGCCTTCTGTGAG
                                                                                             AlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
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03-AJG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-0350666P.
12-APR-2002; 2002US-0372246P.
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C; 927 G; 1338 T; 0 U; 0 Other;
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Human, differential expression, cancer; angiogenic disorder;
fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
                                                                             inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                      Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:151.
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Wilson KE, Zlotnik A;
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Murray R, Watson SR,
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04-AFR-2002; 2002US-0370110P.
15-AFR-2002; 2002US-0372246P.
05-UUN-2002; 2002US-0386614P.
16-UUL-2002; 2002US-0386614P.
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21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0333393P.
14-DEC-2001; 2001US-033534P.
14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0340376P.
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2002US-0347211P.
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2002US-0397845P
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20-FEB-2002;
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22-JUL-2002;
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Mack DH,
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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample. WPI; 2003-468649/44. P-PSDB; ADN38834.

Claim 8; SEQ ID NO 151; 1385pp; English

The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a content by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a colypeptide of the invention; use of such antibodies for drug targeting; colypeptide of the invention; use of such antibodies for drug targeting; colypeptides and nucleic acids. The nucleic acids, polypeptides, and methods are useful for diagnosing, prognoshing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present

ADN38833 standard; cDNA; 4212 BP

ADN38833 ID ADN3 RESULT 3

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 Other;
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liver cancer, is differentially expressed in liver tumors relative to
normal liver tissues.
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                                                                                                                                                                                                                                                                                           "Liver tumour marker protein, CRG-L1"
                                           Human cDNA encoding a liver tumour marker protein, CRG-L1
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                                                                                       Human; ss; gene; liver cancer; liver tumour; CRG-L1;
hepatocellular cancer; chromosome 9p.
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27-JAN-2001; 2001WO-EP000900

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This invention describes novel human ceramidase (I) containing a specific structural motif which has antiproliferative, anticancer, anti-eczema, antipsoriasis and dermatcholgical activity. (I) cleave ceramide, resulting in formation of sphingosine. (I), or the nucleic acid (II) encoding it, are used for diagnosis, prevention or treatment of diseases associated with ceramide defects, particularly altered cell proliferation (cancer) or altered ceramide layers on the skin (neurodermatitis, eczema, psoriasis), also for targeted modification of the permeability barrier by ceramidase or its activators, e.g. for transcutaneous delivery of substances. Specifically they are used for diagnosis of ichthyosis, particularly lamellar ichthyosis ICR2. (I) can also be used in cosmetics. This sequence encodes human ceramidase X3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuPhePhelleLeuProProlleCysMetCysLeuPheArgGlnTyrAlaThrCysPhe
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                                                                                                                                                     New ceramidase containing specific structural motif, useful for diagnosis, prevention and treatment of ceramidase defects, e.g. ichthyosis, also in cosmetics.
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Conservative:
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                                            (MEMO-) MEMOREC MEDICAL MOLECULAR
                                                                                                                                                                                                                        Claim 3; Page 17; 31pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.54e-129
1373.50
94.91%
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2000DE-01003293.
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Indels: Gaps:

	DB:	10
CIGCICALCACAGAGCIAAAAGAGGIGIGACAGCAIGCGIGIGITIAAGCCIGGGCCTCTTC	US-10-017	7-410-2 (1-275) x ADL066
1st Periotytentrylipintreukiaheukheeysimpilessraspainalaheeyssiu 200 	λΌ	37 IleSerAsnValLeuPhe
LeuLeuSerSerPheHisPheProTyrLeuHisCysValTrpHisIleLeulleCysLeu	名 &	179 ATCAGCAATGICTTATTT
CTGCTGTCATCCTTCAACTTCCCCTACCTGCATGCATGCA	7 A	
221 AlaserTyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleFroGlu 240 :::	λο	77 GlySerValTyrPheHis/
241 GlnGlyProValileArgPheTrpProSerGluLysTrpAlaPheileGlyValProTyr 260	qa Xo	299 GGATCCGTCTACTTCCAT
Valser	qa	359 GTCCTTTGGGTTCTGATG
778 GIGTCCCTCTGTGCCAACAAGAATCATCACACAAGACACG	දු දු	117 IlePheArgAsnAspArgC
RESULT 6 ADLOGGAO standard. comma. 1527 no	λo	
	qa	479 ACGTGCCTGGCATTTGTC
06-MAY-2004 (first entry)	ò	գ—
Human 3T3 cell conversion promoter PP11646 cDNA.	q _Q	-
3T3 cell conversion; promoter; human; gene; ss.	δ	
Homo sapiens.	q O	CACAGGAAAGGTGGC
CN1403477-A.	ðo í	168ArgCysAs
19-MAR-2003.	q g	
12-SEP-2001; 2001CN-00126725.	% 1	184 pTrpThrLeuAlaLeuPhe
12-SEP-2001; 2001CN-00126725.	gg (
(SHAN-) SHANGHAI XINSHIJIE GENE TECHN DEV CO LTD.	à á	204 rPheHisPheProTyrLet
Gu J, Yang S;	g i	
WDI; 2003-494226/47. P-PSDB; ADLO6641.	3 8	839 AAAGCACACTTTGTAAAA
Human protein with function of promoting 3T3 cell conversion and its coding sequence.	λŏ	214
Example 1; SEQ ID NO 1; 41pp; Chinese.	QΩ	899 GCCTGATTGTCATGCTTAC
This invention describes a novel human protein with 3T3 cell conversion	δ t	
recombinant process of producing the polypeptide. The present invention also discloses the agonist resisting the polypeptide. The present invention	a à	215
effect. The present invention also discloses the application of the polynucleotides encoding the human protein with 3T3 cell conversion promoting function.	qq	1019 GAAGAGGCCCCTGGGCTG
Sequence 1527 BP; 376 A; 357 C; 383 G; 411 T; 0 U; 0 Other;	<i>አ</i> ස	223 TyrLeuGlyCysValCys
Alignment Scores: 3.05e-102 Length: 1527	3 &	
Matches:		

an	3-10-017-410	-2 (1-275) x ADL06640 (1-1527)
δ		lleSerAsnValLeuPhePhelleLeuProProlleCysMetCysLeuPheArgGlnTyr 5
qq	,	ATCAGCAANGTCTTATTTTTTTTACCGCCCATCTGCATGTGCTTGTTTCGTCAGTAT 2
\$ B	57	AlaThrCysPheAsnSerGly11eTyrLeu11eTrpThrLeuLe
ò		GlysevalTyrPheHisAlaThrieuSerPheLeuGlyGlmMetLeuAspGluLeuAla 9
q ₀	29	GGATCCGTCTACTTCCATGCAACCCTTAGTTTCTTGGGTCAGATGCTTGATGAACTTGCA 35
ò	6	IleLeuTrpValLeuMetCysAlaLeuAlaMetTrpPheProArgArgTyrLeuProLys
ద	35.	GICCITIGGGITCTGAIGHGHGHTGCTTTGGCCAIGHGHTCCCCAGAAGGIAICTACCAAAG 41:
ò	, 117	IlePheArgAsnAspArgGlyArgPheLysAlaValValCysValLeuSerAlaIleThr
đ	,	ATCTTTCGGAATGACCGGGGTAGGTTCAAGGTGGTGGTCAGTGTCCTGTCTGCGGTTACG 478
ð		ThrCysLeualaPheIleLysProAlaIleAsnAsnIleSerLeuMetIleLeuGlyLeu 15
අ		ACGIGCCIGGCATITGICAAGCCIGCCATCAACAACAICTCICIGAIGACCCIGGGAGIT 538
õ		ProcysThrAlaLeuLeuValAlaGluLeuLys
đ	-	CCTTGCACTGCACTGCTCATCGCAGAGCTAAAGAGGCATGAGAGGAACCAGCGAAGGAGA 598
õ	,,	167
đ		CACAGGAAAGGTGGCCAGCAAGGAGGTGGAGACAAGGTCTGACGATGAGTGACTCTCTGG 658
ò	,,	ArgCysAspAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTr 184
qa	ŭ	ACCCCCGTGCAGGTGTGACAACATGCGTGTGTTTAAGCTGGGCCTCTTCTCGGGCCTCTG 718
ò		PTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSe
q	•	GTGGACCCTGGTTCTGCTGGTTGCTGGTGACCGAGCTTTCTGCGAGCTGTTGTCTT
ò		rPheHisPheProTyrLeuHisCysValTrp214
qq	•	CITCAACTICCCCTACCTGCACTGTGTGTGGACGGTCAGATGGTTCAGAAGCCACTG 838
ð	.,	214
d	_	AAAGCACACTTTGTAAAAAGCTGAATTGACTCCAGGGAGCAGGCTTAGCCGGAACGAAAG 898
ð	.,	214
qq	_	GCCTGATTGTCATGCTTAGCAGGACTATTTAAGAACATTCTAAAACGGGTCCCCAAATTGC 958
õ	.,	
q		TGAAGATTTATCATCCTGCTATTCCAGGGATTGTTGGTAATCTTCATCCTTTCCTAATTA 1018
ờ		HisleLeulleCysLeuAlaSer 222
q	ਜ	GAAGAGGCCCCTGGGCTGCAACTACAGTCAGCAAGGCACATCCTCATCTGCTGCTTGCT
ð	.,	TyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGluGlnGly 242
đ	10	TACCTGGGCTGTGTATGCTTTGCCTACTTTGATGCTGCCTCAGAGATTCCTGAGCAAGGC 11
à	. 243	ProvalileArgPheTrpProSerGluLysTrpAlaPheIleGlyValProTyrValSer 2
A A	11	CTGTCATCAAGTTCTGGCCCAATGAGAAATGGGCCTTCATTGGTGTCCCCTATGTGTCC 11

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1078
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                                                                                                                                              ThrCysLeuAlaPhelleLysProAlalleAsnAsnIleSerLeuMetIleLeuGlyLeu 156
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GGATCCGTCTACTTCCATGCAACCCTTAGTTTCTTGGGTCAGATGCTTGATGAACTTGCA 358
                                                                                   | IlePheArgAsnAspArgGlyArgPheLysAlaValValCysValLeuSerAlaIleThr
                                                                                                  -----HisIleLeuIleCysLeuAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1079 TACCTGGGCTGTGTATGCTTTGCCTACTTTGATGCTGCCTCAGAGATTCCTGAGCAAGGC
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                                                                                                                                                                                                                                                                                                                     -----ArgCysAspAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTr
                                                                                                                                                                                                                                                                                                                                        ACCCCGTGCAGGTGTGACAACATGCGTGTTTTAAGCTGGGCCTCTTCTCGGGCCTCTG
                                                                                                                                                                                                                                                                                                                                                                              pTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSe
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                                                         Greetriegetrergargrefrererriegeceargregrreeceagaaggrareraaag
                                                                                                                                                             ACGIGCCTGGCATTTGTCAAGCCTGCCATCAACAACAACATCTCTGATGACCCTGGGAGTT
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                                                                                                                                                                                                    ProCysThrAlaLeuLeuValAlaGluLeuLys-----
                                                                                                                                                                                                                                                                                                                                                                                                                                         rPheHisPheProTyrLeuHisCysValTrp-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel human protein with 3T3 cell conversion promoting function, polynucleotides encoding the polypeptide and the recombinant process of producing the polypeptide. The present invention also discloses the agonist resisting the polypeptide and its treatment effect. The present invention also discloses the application of the polynucleotides encoding the human protein with 3T3 cell conversion promoting function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 GCAACATGCTTCAACAGTGGCATCTACTTAATCTGGACTCTTTTGGTTGTAGTGGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 AlaThrCysPheAsnSerGlyIleTyrLeuIleTrpThrLeuLeuValValValGlyIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein with function of promoting 3T3 cell conversion and coding sequence.
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222
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116
 LeuLeuCysAlaHisLysLysSerProValLysIleThr 275
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                         conversion; promoter; human; gene;
                                                                                                                                                                           Human 3T3 cell conversion promoter PP11646
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SHAN-) SHANGHAI XINSHIJIE GENE TECHN DEV
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1110.50
66.20%
62.54%
73.45%
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                                                                                       DNA; 1527
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                                                                                                                                              (first entry)
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                                                                                       standard;
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Best Local Similarity:
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81 PheHisAlaThrLeuSerPheLeuGlyGlnMetLeuAspGluLeuAlaIleLeuTrpVal 100
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           61 AsnSerGlyIleTyrLeuIleTrpThrLeuLeuValValValGlyIleGlySerValTyr 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCTCATCACAGAGGTAAAGAGGTGTGACAACATGCGTGTGTTTAAGCTGGGGCCTCTTC
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13-SEP-2002; 2002US-00323739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
                      bone cartilage tissue growth; tendon tissue growth;
ligament tissue growth; nerve tissue growth; regeneration; wound healing;
tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;
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Wang D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluAspAsnTyrThrIleValProAlaIleAlaGluPheTyrAsnThrIleSerAsnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of burns, incisions and ulcers, and in treating cancer. The sequence represents CDNA encoding a novel human protein.
                                                                                                                                                                                                                                                                                                                                                                                                        RW, Ren F, Zhang J, Zhao QA, Wang
Weng G, Zhou P, Drmanac RT, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1623 BP; 305 A; 457 C; 382 G; 479 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               887 TTATTTTTCATTTTACCGCCCCATCTGCATGTGCTTGTTTCGTCAA--
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Matches:
Conservative:
Mismatches:
Indels:
myeloid cell disorder; lymphoid cell disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Asundi V, Goodrich
Ghosh M, Xue AJ, Wehrman T,
Haley-Vicente D;
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77.09%
72.00%
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13-SEP-2002; 2002US-00323739
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Best Local Similarity:
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                                                                                                                                                                     WO2003025148-A2
                                                                                                                             Homo sapiens
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Query Match:
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(first entry)

06-NOV-2001

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The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents a novel human expressed sequence tag, EST.
                                                                                                                                                                   New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement.
                  Wang J;
Wang D;
                  Zhang J, Zhao QA,
ou P, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 A; 138 C; 131 G; 134 T; 0 U; 3 Other;
                  Goodrich RW, Ren F, Zhang
Wehrman T, Weng G, Zhou P,
                                                                                                                                                                                                                                                                                         Example 2; SEQ ID NO 719; 156pp; English.
                     Asundi V,
                                                                                                         2003-354603/33
                                Haley-Vicente D;
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                                                                                                                                P-PSDB; ADI21688
                     Tang YT,
Ghosh M,
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Length:
Matches:
Conservative:
Mismatches:
Indels: 1.12e-49 584.00 98.17% 96.33% 38.62% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match:

US-10-017-410-2 (1-275) x ADI21468 (1-487)

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1 MetGlyAlaProHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys
                ATGGGCCCCCCCCCCCACTGTGCACCACCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGC
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                                                              GluAspAsnTyrThrIleValProAlaIleAlaGluPheTyrAsnThrIleSerAsnVal
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AAK51566 standard; cDNA; 1215

AAK51566

AAK51566 ID AAKS XX AC AAK5 XX

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production of other cytokines in other cell populations. The pholynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. atem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SBQ ID NO 2110 (AAKS2SB1), 2111 (AAKS2SB2) and 3666 (AAMS0020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like activities, useful
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                                                                                                                         Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, ao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1215 BP; 213 A; 374 C; 309 G; 319 T; 0 U; 0 Other;
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                                                            Human polynucleotide SEQ ID NO 111.
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20-UTW-2000; 2000US-00598075.
19-UTW-2000; 2000US-0062325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0065561.
20-OCT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00728422.
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Ma Y, Zhao QA,
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Nucleic acids encoding polypeptides with cytokine-like activities, useful

Claim 1; Page 4462; 6221pp; English.

diagnosis and gene therapy

in

2001-476283/51.

WPI; 2001-476283/: P-PSDB; AAM79417.

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Wang

u C, Cao) Chen R, V

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Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xi Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Xue AJ, Yang Y, Wejhrman T, Goodrich R;

(HYSE-) HYSEQ INC Tang YT, Liu C Ma Y, Zhao QA,

03-FEB-2000; 2000US-00496914.
27-AFR-2000; 2000US-00560875.
20-UUN-2000; 2000US-00590075.
19-UUL-2000; 2000US-00654936.
15-SER-2000; 2000US-0065561.
20-CT-2000; 2000US-0063325.
30-NOV-2000; 2000US-00728422.

05-FEB-2001; 2001WO-US004098

WO200157190-A2

09-AUG-2001

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, call proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID No 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor, immunomodulatory, cancer, leukaemia, nervous system disorder, arthritis, inflammation, ss.

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Human polynucleotide SEQ ID NO 2079.

(first entry)

06-NOV-2001

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This invention describes novel human ceramidase (I) containing a specific structural motif which has antiproliferative, anticancer, anti-eczema, antipsoriasis and dermatcholgical activity. (I) cleave ceramide, resulting in formation of sphingosine. (I), or the nucleic acid (II) encoding it, are used for diagnosis, prevention or treatment of diseases associated with ceramide defects, particularly altered cell proliferation (cancer) or altered ceramide layers on the skin (neurodermatitis, eczema, psoriasis), also for targeted modification of the permeability barrier by cubstances. Specifically they are used for diagnosis of ichthyosis, particularly lamellar ichthyosis ICR2. (I) can also be used in cosmetics. This sequence encodes human ceramidase XI
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                                                                                                                                                                                                                                     treatment
                                                                                                                                                                                                                                                                                                                            Claim 3; Page 16; 31pp; German.
                                                                                                                                                                                                                                                                    ichthyosis, also in cosmetics.
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549.50
59.38%
40.23%
                                                                                                                                                                                                         New ceramidase containing
diagnosis, prevention and
                                                       Conradt
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P-PSDB; AAB86363.
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                                                       Hofmann K,
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US-10-017-410-2 (1-275) x ABL24043 (1-537)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175-ABL30511), processed DNA ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                    208 oTyrieuHisCysValTrpHisIleLeuileCysLeuAlaSerTyrLeuGlyCysValCy 228
                                                                     228 sPheAlaTyrPheAspAlaAlaSerGluIleProGluGlnGlyProValIleArgPheTr 248
                                                                                                                              CATGGCCTTGGTGGATGCCAACTATGAGATGCCAGGTGAAACCCTCAAAGTCCGCTACTG 728
aLeuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPhePr 208
                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide SEQ ID NO 23602.
                                                                                                                                                                pProSerGluLysTrpAlaPheIleGlyValProTyrValSerLeu 263
                                                                                                                                                                                GCCTCGGGACAGTTGGCCC---GTGGGGCTGCCTACGTGGAAATC 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myers EW;
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11-JUL-2000; 2000US-00614150
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Conservative: Mismatches: Indels: Gaps:

Length: Matches:

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Best Local Similarity: Query Match: DB:

Percent Similarity:

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                                                                                                                                                                                                                                                   MetTrpPheProArgArgTyrLeuProLysIlePheArgAsnAspArgGlyArgPheLys 126
                                                                                                                                                                                                                                                                                                                                               127 AlaValValCysValLeuSerAlaIleThrThrCysLeuAlaPheIleLysProAlaIle 146
                                                                                                                                                                                                                                                                                                                                                                                                         AgnAsnIleSerLeuMetIleLeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeu 166
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                                                                                                                 47 ProlleCysMetCysLeuPheArgGlnTyrAlaThrCysPheAsnSerGlylleTyrLeu 66
                                                                                                                                                                             86
                     49 TOGGAGCACCTAAGACCCGGAAGCTCGCCGTCGACTGGTGGGAAGAGCAACTACTTGATT
                                                                          109 TCGTCCAACATCGCGAGTTCGTGAACACGTTTAGCAACTTCCTGTTCATCCTACTGCCG
                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
7 TrpAspHisLeuArgAlaGlySerSerGluValAspTrpCysGluAspAsnTyrThrlle
                                                         27 ValProAlaIleAlaGluPheTyrAsnThrIleSerAsnValLeuPhePheIleLeuPro
                                                                                                                                                                         67 IleTrpThrLeuLeuValValValGlyIleGlySerValTyrPheHisAlaThrLeuSer
                                                                                                                                                                                          Drosophila; developmental biology; cell signalling; insecticide;
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Myers EW;

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23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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                                                                                                                   Adams M,
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                                                                                                                                                                                          interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ile---ThrThrCysLeuAlaPheIleLysProAlaIleAsnAsnIleSerLeuMetIle 153
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                                                                                                                                                                                                                                                                                                38 SerAsnValLeuPhePheIleLeuProProIleCysMetCysLeuPheArgGlnTyrAla 57
                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBC01840-ABL16175) and the encoded proteins (ABBC01737-ABBC2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                               ThrCysPheAsnSerGlyIleTyrLeuIleTrpThrLeuLeuValValValGlyIleGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orosophila melanogaster genomic polynucleotide SEQ ID NO 42769
                                                                                                                                                      Sequence 4758 BP; 1304 A; 981 C; 980 G; 1493 T; 0 U; 0 Other;
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Drosophila melanogaster.

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                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1676-ABL30511), expressed DNA sequences (ABL16775) and the encoded proteins (ABBS7737-ABR27272). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 4071 BP; 1027 A; 938 C; 941 G; 1165 T; 0 U; 0 Other;
                                                                                                                                Claim 1; SEQ ID NO 42769; 21pp + Sequence Listing; English.
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Mismatches:
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11, Ap. 3254, Ap. 57, Appl

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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_Lgenes Version 2.0
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Patent No. 6783969
GENERAL INFORMATION:
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Ma, Yunging
Yamazaki, Victoria
Chen, Rui-hong
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Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
Ren, Feiyan
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Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
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Yang, Yonghong
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42. /cgn2_6/ptodatca/l/ina/PCTUS_COMB.seq:*
65. /cgn2_6/ptodatca/l/ina/PcTUS_COMB.seq:*
66. /cgn2_6/ptodatca/l/ina/backfiles1.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-621-976-11241
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US-09-252-991A-892
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US-09-792-616-1
US-09-328-352-577
US-09-710-279-4182
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TYPE: DNA
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                                                                                                                                                                                                                                    34 TyrasnThrIleSerasnValLeuPhePheIleLeuProProIleCysMetCysLeuPhe
                                                                                                                                                                                                                                                                                           54 ArgGlnTyrAlaThrCysPheAsnSerGlylleTyrLeuleTrpThrLeuLeuValVal
                                                                                                                                                                                                                                                                                                              74 ValGlyIleGlySerValTyrPheHisAlaThrLeuSerPheLeuGlyGlnMetLeuAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 ValCysPheAlaTyrPheAspAlaAlaSerGluIleProGluGlnGlyProValIleArg
                                                                                                                                                                                 14 SerSerGluValAspTrpCysGluAspAsnTyrThrIleValProAlaIleAlaGluPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 GTCTTTACATTAGTACTTCGATCTATATATTGTTACATGGGTTTATCCATGGCTTAGA
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                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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734 TATAGGCCAAAAGTGAAGTTTCTCTTT
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2.09-621-976-11241/c
; Sequence 11241, Application US/09621976
; Patent No. 6639063
                                                     1.5e-14
209.50
40.89%
30.11%
13.86%
; LOCATION: (2)..(802)
US-09-799-451-875
                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                          Alignment Scores
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JAMEAN INFORMATION: Weinstock et al TITLE OF INVENTION: Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: 107195.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 1441
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|145 TIGAATACTACCACTAACTCAGTATTTATTGCTTTGGCAAC-ATTTGCGATATATCATGC 203
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Mismatches:
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Pro-
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
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Matches:
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; Sequence 1441, Application US/09248796A
; Paten No. 6747137
; GENERAL INFORMATION:
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173.00
40.64%
27.09%
11.44%
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204.00
97.30%
91.89%
13.49%
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                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
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US-09-248-796A-1441
                                                                                                                                                                 SEQ ID NO 11241
LENGTH: 358
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ATTORNEY/AGENT INFORMATION: NAME: Collins, John M. REGISTRATION NUMBER: 26,262 REFERENCE/DOCKET NUMBER: 25043-A TELECOMMUNICATION INFORMATION: TELEPONE: 816/474-9050 TELEPAX: 816/474-9050 TELEPAX: 816/474-9050 SEQUENCE CHARACTERISTICS: LENGTH: 6755 base pairs TYPE: nucleic acid STRANDENNES: double TOPOLOGY: unknown MOLECTLE TYPE: DNA (genomic) HYPOCHETICAL: NO MOLECTLE TYPE: DNA (genomic) HYPOCHETICAL: NO MOLECTLE TYPE: DNA (genomic) MYPOCHETICAL: NO MOLECTLE TYPE: DNA (genomic) STRAIN: SCHOUCE: CRIGANISM: Staphylococcus aureus STRAIN: UT0007	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Ouery Match: 3.1.9\$ Mismatches: Mismatches: Best Best Best Best Best Best Best Best	-10-017-410- 42 3259 54 3199 74 3148	3088 CCCCCTTTGCTGCTGCTGGTTCG 87 PheLeuGlyGlnMetLeuAspGl1 3028 CTGCTTGTGTCCCTCTTTTTCT 107 MetTrpPheProArgArgTyrLei 2968 TCTTTTTCTCTCTCTGGTGG 126
Oy 32 LeuPheArgGlnTyrAlaThrCysPheAsnSerGlylleTyrLeuIleTrpThr-LeuLe 71	QY 144 OALAILEASNASNILESELLEUMETILELEUGIYLEUPTOCYSTHrALALEULEUVA 163 :::	174 1PheLysLeuGlyLeuPheSerGlyLeuTrpThrLeuAlaLeuPheCysTrp11eSe	RESULT 4 US-08-931-999-4/C US-08-931-999-4/C Sequence 4, Application US/08931999 Patent No. 604319 GENERAL INFORMATION: PAPPLICANT: Indealo, John J. APPLICANT: Crupper, Scott S. TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: Hovey, Williams, Timmons & Collins STREET: 2405 Grand Boulevard, Suite 400 CITY: Kansas City STATE: Missouri CITY: Kansas City STATE: Missouri COWNTRY: U.S.A. ZIP: 64108 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: PatentIn Release #1.0, Version #1.30 SOFTWARE: PatentIn Release #1.0, Version #1.30 FILING DATE: APPLICATION NUMBER: US/08/931,999 FILING DATE: CLASSIFICATION DATA: APPLICATION NUMBER: US 08/710,561 FILING DATE: 19-SEP-1996

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ys-----Leuphe 53
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TrGrGTTCCCCCTTCTTTTCCTT 3149
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| IGTGTTTTCCTGTCCCGCTGCCC 3029
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CCTTCTTCCTTTTT----- 2708
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6755
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109 PheProArgArgTyrLeu 782 TTCAGCCGGGGTACCTCTACACCC 123 GlyArgPheLysalaValValCysV 842 GGCTGCTGCTGCGGCTGGTGGTCC 143 LysProAlalleAsn 155 GlyLeuProCysThrAlaLeuLeuV 155 GlyLeuProCysThrAlaLeuLeuV 155 GlyLeuProCysThrAlaLeuLeuV 155 GlyLeuProCysThrAlaLeuLeuV 155 GlyLeuProCysThrAlaLeuLeuV 155 GlyLeuProCysThrAlaLeuLeuCGCCT 175 PheLysLeuGlyLeuPheSerGlyL 175 FheLysLogTCGCCAGGCCTGCCTGCCCCC 175 AspGlnAlaPheCysGluLeuLeuS 176 GlyLeuLleCysLeuAlaSerT 176 Cortact Cortact Cortact 187 Application US/09252991 187 Land Cortact 187 Application US/09252991 188 Application US/09252991 189 Applicati	Indels: Gaps: -252-991A-944 (1-2859) -8LeuPheArgGlnTyrAlaThr- FTAC-TTCAGCACCTACGGGCCF
200 SerbheHispheProTytleu	Db 542 CTGATGGGCCTTCTACGGGGTGCTTCTGGGTTCTGCTACAACCTG 601 Qy 63 GlylleTyrLeu

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APPLICANT: PXE Incernational, Inc.
APPLICANT: DXI Incernational, Inc.
APPLICANT: University of Hawaii
TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (WRP6) causing
TITLE OF INVENTION: Pseudoxanthoma Blasticum
FILE REFERENCE: PXE-001
CURRENT APPLICATION NUMBER: US/09/792,616
CURRENT FILING DATE: 2011-02-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
                                                                       1377 TTCCCGCGCCTCGACCGCTTCCTCCGCGGCCTGCTGCTGCGCGTGGTCGTCCTGTTGGCC 1318
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------GAGCCGCTGGGGGCTGCGCCTGGAACGTC 1282
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                                                    TyrLeuIleTrpThrLeuLeuValValValGly1leGlySerValTyrPheHisAlaThr
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                                                                                                                          LeuSerPheleu-----GlyGlnMetLeuAspGluLeuAlaIleLeuTrpValLeuMet
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                   US-10-017-410-2 (1-275) x US-09-252-991A-1139 (1-1575)
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OTHER INFORMATION: "n" can be an A or a T
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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LENGTH: 107820
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
SEQ ID NO 1139
LENGTH: 1575
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                                                                                      ctggcctgttttcgccagcttgacgcctgctttaagctgctgccggacacgtg 795
                                                                                                                                                        GlyArgPheLysAlaValValCysValLeuSerAlaIleThrThrCysLeuAlaPheIle 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 HislleLeulleCysLeuAlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAla 234
                                                                                                                                   LeuAspGluLeuAlaIleLeuTrpValLeuMet------CysAlaLeuAlaMetTrp 108
                                                                                                                                                                                                           --ProLysIlePheArgAsnAspArg 122
                                                                                                                                                                                                                                                                                                                                            -----AsnIleSerLeuMetIleLeu 154
                                                                                                                                                                                                                                                                                                                                                                                                             155 GlyLeuProCysThrAlaLeuLeuValAlaGluLeuLysArgCysAspAsnValArgVal 174
                              376 ITCCTCTTCGTCTCGCTACGCGAGGCCACCTATGCCTGGTACCTGCTGTACAACCTCAGC 735
                                                              74 ValGlyIleGlySerValTyrPheHisAlaThrLeuSerPheLeu-----GlyGlnMet
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; Sequence 1139, Application US/09252991A
; Patent No. 6551795
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Best Local Similarity:
Query Match:
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1165 AGC 1167
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ORGANISM: Acinetobacter baumannii
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                              US-09-328-352-577
                                                                 Alignment Scores:
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Retent No. 6562958

GRNERAL INFORMATION:
GRNERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 577
LENGTH: 1794
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                                                                    38349 ATAATGTTGCTGTTTTTCTTACTGTTACATTGCCATGTTGCTATTCCGTTACTATAATTTC 38408
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                                               19 TrpCysGluAspAsnTyrThrlleValProAlalleAlaGluPheTyrAsnThrlleSer
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                  US-10-017-410-2 (1-275) x US-09-792-616-1 (1-107820)
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97 AGTATTTTGTACTTAATTGCTGCTAATTGGTTGATGCTTCCAGATAGCATTCAACTCATT 156
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT PAPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
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; Sequence 4182, Application US/09710279
; Patent No. 6703492
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                                                                                                OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
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                                                              TYPE: DNA ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 3304
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98.50
34.42%
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Sequence 2470, Application US/09248796A

Sequence 2470, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANF

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PILING DATE: 1099-02-12

CURRENT PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

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:::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | :::|| | 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291 TATTTTGATTTCGCTTGTT
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ORGANISM: Candida albicans
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Best Local Similarity:
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Sequence 16. Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

ITILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 3840
:::|||
39610 G----TTATGGCAAGCAGGATTTTGGTTG---TCATTTATTGCCGTGTTGTTATTGAT 89660
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                                                                                                                                                150 rLeuMetIleLeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeuLysArgCysAs 170
                                                                                                                                                                                                                               170 pAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTrpTrpThrLeuAlaLeuPh 190
                                                                                                                                                                                                                                                                                                                                                                                            210 uHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCysPheAl 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SerGluIleProGluGlnGlyProVa 244
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                                                                132 uSerAlaIleThrThrCysLeu-----AlaPheIleLysProAlaIleAsnAsnIleSe
                                                                                          936 GTATCAATTGGCAGG---TATTTC------GCATTTGCTTGCCATTTCAGGGAC
                                                                                                                                                                                                                                                                                                               190 eCysTrplleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPheProTyrLe
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                                                                                                                                                                                         ----GCAGCTTGGCTGGTTCGCTACTTA
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Matches:
Conservative:
Mismatches:
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38.68%
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89589 GATTTGGCTTGAC---
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89505 TTTATTAATT-
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Best Local Similarity:
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APPLICANT: Batterson, Chandra
APPLICANT: Berterson, Chandra
APPLICANT: Berterson, Chandra
TITLE OF INVENTION: MUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US(99/596,002
CURRENT FILING DATE: 1999-06-16
PRIOR APPLICATION NUMBER: 60/140,121
NUMBER: OF SEQ ID NOS:
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SOFTWARE: PARIOR PROGRAM
TYPE. N.**
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    -LeuGlyLeuProCysThrA 160
                       :|||:::||| :::|||
444 CATIGCCITGGGTGATAACACGCTITGTGTTATTGTTTTTATTAACAGTTTGTTGCA
                                                                                                                                                                                           ||||:::|||
---TGTTTCATATTCGATAGTTGCAAAGAG
                                                                                                                                                                                                                                                                                                                                218 IleCysLeuAlaSerTyrLeuGlyCys---ValCys-PheAlaTyrPheAspAlaAlaSe
                                                                                                                                                                                                                                                                                                                                                                                                                  236 rGluIleProGluGlnGlyProValIleArgPheTrpProSerGluLysTrpAlaPheIl
                                                                                   160 laLeuLeuValAlaGluLeuLysArgCysAspAsnValArgValPheLysLeuGlyLeuP
                                                                                                                          504 GGTTGTTTTGTATGCCCCTTATCAATTGTTTTTCTGTTATGTGATATCGGGTGATCCTAT
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Mismatches:
Indels:
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Matches:
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720 TGGATTGTTGTACTATTATTGTT 744
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US-09-596-002-36
Sequence 36, Application US/09596002
Patent No. 6632636
GENERAL INFORMATION:
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OTHER INFORMATION: Incyte
PUBLICATION INFORMATION:
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684 TAAGTTG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SerGlyLeuTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCys--- 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 LeuLeuValAlaGluLeuLysArgCysAspAsnValArgValPheLysLeuGlyLeuPhe
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                              63:
                                                                                                                                           TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
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; Sequence 63, Application US/08781986A
; Patent No. 6737248
  (240) 314-1224
                     TELEFAX: (301) 309-8439 INFORMATION FOR SEQ ID NO: 63: SEQUENCE CHARACTERISTICS:
                                                                                LENGTH: 8155 base pairs
                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charles Kunsch
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    TELEPHONE:
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APPLICANT: Charle
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.041 TGCACAAACACATTTATGCACATTTGCCAAGATGGCAAATTCGTATGATGGTCATGGTGTT 1100
                                                                                                                                                                                                                                            -----ATACTGCCCACTGGCATGATTTCTGTGCTGGCGTGGGTAGCCTTGTTGAT 1244
                                                                                                                                                                                                                                                                                       210
                                                                                                                                                                                                    pAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTrpTrpThrLeuAlaLeuPh 190
                                                                                                                                                                                                                                                                                                                                                                   210 uHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCysPheAl 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- TrpAlaPheIleGlyValPr 259
                                                                                                                                                                                                                                                                                                                                                                                                             1266 G-----TTATGGCAAGCAGATTTTGGTTGTCATTTATTGCCGTGTTGTTATTGATGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uSerAlaIleThrThrCysLeu-----AlaPheIleLysProAlaIleAsnAsnIleSe
                                                                              1101 GGCAAGTTTGGTTTATGCGTTGTTTACAGGGTTTGATGTGCCTGCGGTGCGAACTGTTTA
                                                                                                                      rLeuMetIleLeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeuLysArgCysAs
                                                                                                                                                                                                                                                                                     190 eCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPheProTyrLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----GinGlyProValileAr
                                                                                                                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Poly
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
ADDRESSES: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1440 ACCTGTGTCTATCTTATTTGGCAAGGTATCA 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-OCE-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: MARK J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTyrValSerLeuLeuCysAlaHisLysLysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gPheTrpProSerGluLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 SerAsnValLeuPhePheIleLeuProProIleCysMetCysLeuPheArg----GlnTyr 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AlaThrCys-----PheAsnSerGlyIleTyrLeuIjeTrpThrLeuLeuValValVal 74
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CORRESPONDENCE ADDRESS:
ADDRESSER: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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45
24
107
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                            FILING DATE:

CLASSIFICATION 435

CLASSIFICATION 435

FILING DATE:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: PP248PP

RECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8514

TELEPHONE: (301) 309-8514

INFORMATION FOR SEQ ID NO: 63:

SEQUENCE CHARACTERISTICS:

LENGTH: 8155 base pairs

TYPE: mucleic acid

STRANDENNES: double
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20.45%
6.42%
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Best Local Similarity:
Query Match:
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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Sequence 1999, Ap Sequence 1645, Ap Sequence 30658, A Sequence 2014, Ap Sequence 2014, Ap Sequence 1773, Ap Sequence 12701, Ap Sequence 1369, Ap Sequence 2099, Ap Sequence 2099, Ap Sequence 2099, Ap Sequence 2099, Ap Sequence 2099, Ap Sequence 2099, Ap Sequence 2099, Ap Sequence 2099, Ap Sequence 2099, Ap
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Publication No. US20020115094A1

GENERAL INFORMATION:
APPLICANT: Farnham, Peggy J

APPLICANT: Graveel, Carrie R

TITLE OF INVENTION: Polymouleotide Differentially Expressed in Liver Cancer
FILE REFERENCE: 960296.97401

CURRENT APPLICATION NUMBER: US/10/017,410

CURRENT FILING DATE: 2001-12-14

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1
                                                                     Sequence 21, Appl
Sequence 151, App
Sequence 3, Appli
Sequence 6, Appli
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Sequence 32295, A
Sequence 107231,
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                                                                     US-10-188-832-21
US-10-295-027-151
US-10-182-447-6
US-09-945-527-48
US-10-182-447-4
US-10-182-447-4
US-10-425-114-302295
US-10-425-115-107231
US-10-425-115-107231
US-10-425-115-107231
US-10-12261
US-10-12261
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US-10-302-172-875
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US-10 -222-798-2069

US-10 -424-599-34549

US-10 -425-115 111725

US-10 -425-114-35305

US-10 -425-114-35305

US-10 -425-114-35305

US-10 -425-118-77895

US-10 -125-11999

US-10 -292-798-1645

US-10 -087-192-2014

US-10 -087-192-2014

US-10 -017-161-2097

US-10 -198-846-12701

US-10 -198-846-12701

US-10 -292-798-1369

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US-09-984-429-316
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; NAME/KEY: CDS
; LOCATION: (35)..(859)
US-10-017-410-1
Query
                                                                                                                                                        LENGTH: 4175
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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-MAXIEN=200000000 -USER=USI0017410 @CGN 1 1.723 @runat 19112004 133621_19052
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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3182.005 Million cell updates/sec
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                                                                                                                                       November 21, 2004, 07:44:08 ; Search time 467 Seconds
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1: \cgn2_6\prodata/2\pubpna/USO7 PUBCOMB.seq:*
2: \cgn2_6\prodata/2\pubpna/USO7 PUBCOMB.seq:*
3: \cgn2_6\prodata/2\pubpna/USO6 NEW PUB.seq:*
4: \cgn2_6\prodata/2\pubpna/USO6_PUBCOMB.seq:*
5: \cgn2_6\prodata/2\pubpna/USO6_PUBCOMB.seq:*
6: \cgn2_6\prodata/2\pubpna/USO8_PUBCOMB.seq:*
7: \cgn2_6\prodata/2\pubpna/USO8_NEW PUB.seq:*
8: \cgn2_6\prodata/2\pubpna/USO8_NEW PUB.seq:*
9: \cgn2_6\prodata/2\pubpna/USO8_NEW PUB.seq:*
10: \cgn2_6\prodata/2\pubpna/USO9_PUBCOMB.seq:*
10: \cgn2_6\prodata/2\pubpna/USO9_PUBCOMB.seq:*
11: \cgn2_6\prodata/2\pubpna/USO9_NEW PUB.seq:*
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17: \cgn2_6\prodata/2\pubpna/USO9_NEW PUB.seq:*
18: \cgn2_6\prodata/2\pubpna/USO9_NEW PUB.seq:*
19: \cgn2_6\prodata/2\pubpna/USOP_NEW PUB.seq:*
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10: \cgn2_6\prodata/2\pubpna/USOP_PUBCOMB.seq:*
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1 MGAPHWWDHLRAGSSEVDWC.....IGVPYVSLLCAHKKSPVKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7255776
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                             nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Jatabase

92688, A 3107, Ap

615, App 35305, A 77895, A

34549, A 111725,

875, App 77897, A

5, Appli

Appli

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; TYPE: DNA
; ORGANISM: Homo
US-10-188-832-21
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Pred. No.:
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                                                                                                        1 MetGlyAlaProHisTrpTrpAspHisLeuArgAlaGlySerGluValAspTrpCys
                                                                                                                                                   GluAspAsnTyrThrIleValProAlaIleAlaGluPheTyrAsnThrIleSerAsnVal
                                                                                                                                                                                                                                    AsnSerGly11eTyrLeuIleTrpThrLeuLeuValValValGly11eGlySerValTyr
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                              Conservative:
Mismatches:
Indels:
Gaps:
                                                                                   US-10-017-410-2 (1-275) x US-10-017-410-1 (1-4175)
           Length:
Matches:
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; Sequence 21, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
    4.29e-157
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100.00%
                            Percent Similarity:
Best Local Similarity:
Query Match:
Alignment Scores:
Pred. No.:
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APPLICANT: Aziz, Natasha

APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002330US
CURRENT APPLICATION UNMERS: US 60/302,814
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: US 60/343,705
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/372,246
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Query Match: 94.78% Indels: 0 DB: 15 Gaps: 0 US-10-017-410-2 (1-275) x US-10-295-027-151 (1-4212) Qy 1 MetGlyAlaPrOHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys 20 Qy 1 MetGlyAlaPrOHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys 20 Db 87 AlGGGCGCCCCGCACTGGTGGAGCTGCAGGCTGGTAGCTGGAGGTGGACTGGTGC 146	Qy 21 GluAspAsnTyrThrIleValProAlaileAlaGluPheTyrAsnThrIleSerAsnVal 40		81 PheHisAlaThrLeuSerPheLeuGlyGlnMetLeuAspGluLeuAlaIleLeuTrpVal 10 	Oy 101 LeuMet CysAlaLeuAlaMet TrpPheProArgArgTyrLeuProLysIlePheArgAsn 120	Qy 121 AspargGlyArgPheLysAlaValValValCsValLeuSerAlaIleThrThrCysLeuAla 140	Qy 141 PhelleLysProAlalleAsnAsnIleSerLeuMetIleLeuGlyLeuDroCysThrAla 160	Qy 161 LeuLeuValAlaGluLeuLysArgCysAspAsnValArgValPheLysLysLeuGlyLeuPhe 180	Qy 181 SerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrp11eSerAspGlnAlaPheCysGlu 200	Qy 201 LeuLeuSerSerPheHisPheProTyrLeuHisCysValTrpHisIleLeuIleCysLeu 220	Qy 221 AlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGlu 240	Qy 241 GlnGlyProVallleArgPheTrpProSerGluLy6TrpAlaPhelleGlyValProTyr 260	Qy 261 ValSerLeuLeuCysAlaHisLysLysSerProVallyslleThr 275	RESULT 4 US-10-017-410-3 ; Sequence 3, Application US/10017410 ; Publication No. US20020115094A1 ; CENERAL INFORMATION: ; APPLICANT: Farnham, Peggy J	; APPLICANT: Graveel, Carrie R; ; TITLE OF INVENTION: Polynucleotide Differentially Expressed in Liver Cancer; FILE REFERENCE: 960296.97401; CURRENT APPLICATION NUMBER: US/10/017,410; CURRENT FILING DATE: 2001-12-14; NUMBER OF SEQ ID NOS: 4
	Db 737 GCTGCCTGGGCTGTATAGCTTTGATGATGCTTGATGATGCTGAGATTCCTGAG 796 Qy 241 GlnGlyProVallleArgPheTrpProSerGluLysTrpAlaPheIleGlyValProTyr 260	Oy 261 ValSerLeuLeuCysAlaHisLysLysSerProValLysIleThr 275	US-10-295-027-151 ; Sequence 151, Application US/10295027 ; Publication No. US20030232350A1 ; GENERAL INFORMATION:	APPLICANT: Aziz, Matasha ; APPLICANT: Aziz, Wendy M. APPLICANT: Ginsberg, Wendy M. ; APPLICANT: Gish, Kurt C. ; APPLICANT: Glavme Richard	APPLICANT: Hevezi, Peter A. APPLICANT: Mack, David H. APPLICANT: Murray, Richard	AFFILCANT: BOS Biotechnology, Inc.; AFFILCANT: BOS Biotechnology, Inc.; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer; FITE DEPENDENT: ASSOCIATION OF SCREENING FOR MODULATORS OF CANCER.	CURRENT APPLICATION NUMBER: US/10/295,027 CURRENT FILING DATE: 2002-11-13 FRIOR APPLICATION NUMBER: US 09/663,733 DEFICE APPLICATION NUMBER: US 09/663,733	FRIOR APPLICATION WUMBER: US 60/350,666 PRIOR FILING DATE: 2001-11-13 PRIOR FILING DATE: 2001-11-13 PRIOR PPPLICATION WUMBER: US 60/335,394	# FILCH APPLICATION WUMBER: US 60/332,464 # PRIOR FILING DATE: 2001-11-21 # PRIOR PPLICATION WUMBER: US 60/334,393 # PRIOR PILING DATE: 2001-11-29	FRICK APPLICATION NUMBER: US 60/340,376 FRICK FILING DATE: 2001-12-14 FRICK APPLICATION NUMBER: US 60/347,211 FRICK APPLICATION NUMBER: US 60/347,211	FRICK APPLICATION NUMBER: US 60/347,349 FRICK FILING DATE: 2002-01-10 FRICK APPLICATION NUMBER: US 60/355,250 FRICK APPLICATION NUMBER: US 60/355,250	FALOR FILING DAIL: 2002-02-08 ; PRIOR APPLICATION NUMBER: US 60/356,714 ; PRIOR FILING DATE: 2002-02-13 ; Remaining Filor Application data removed - See File Wrapper or PALM. NUMBER OF SEOTTH MOS. 1286	NONEX U. S.Y. ID NOS: 1300 SEQ ID NO 151 LENGTH: 4212 T.YPE: DNA ORGANISM: Homo sapiens	Alignment Scores: 2.64e-148 Length: 4212 Pred. No.: 2.64e-148 Length: 256 Score: 1433.00 Matches: 256 Percent Similarity: 98.18% Conservative: 14 Best Local Similarity: 93.09% Mismatches: 5

825

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LeuMetCysAlaLeuAlaMetTrpPheProArgArgTyrLeuProLysIlePheArgAsn 120
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                                                            Sequence 6, Application US/10182447
; Publication No. US20030185814A1
; GENERAL INFORMATION;
APPLICANT: HOFMANN, KAY
; TITLE OF INVENTION: CERAMIDASE
; TITLE REFERENCE: P68055US0
; CURRENT FALIGN UMBER: US/10/182,447
; CURRENT APPLICATION NUMBER: DCT/EP01/00900
; PRIOR FILING DATE: 2002-07-29
; PRIOR FILING DATE: 2001-01-27
; PRIOR FILING DATE: 2000-01-27
; PRIOR FILING DATE: 2000-01-27
; PRIOR FILING DATE: 2000-01-27
; PRIOR FILING DATE: 2000-01-27
; PRIOR FILING DATE: 2000-01-27
; PRIOR SELING DATE: 2000-01-27
; PRIOR FILING DATE: 2000-01-27
; RUMBER OF SEQ ID NOS: 14
; SOFTWARE: PALENTIN VET. 2.1
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1373.50
94.91%
89.45%
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US-10-182-447-6
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Best Local Similarity:
Query Match:
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Mismatches:
Indels:
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Matches:
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1404.00
96.73%
91.27%
92.86%
                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                    ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(825)
US-10-017-410-3
                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
SOFTWARE: Patentin SEQ ID NO 3
LENGTH: 828
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103
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                     Sequence 4, Application US/10182447

Publication No. US20030185814A1

GENERAL INPORMATION:

APPLICANT: HOPPANIN, KAY

TITLE OF INVENTION: CERAMIDASE

FILE REFERENCE: P68055USO

CURRENT APPLICATION NUMBER: US/10/182,447

CURRENT FILING DATE: 2002-07-29

PRIOR FILING DATE: 2001-01-27

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-01-27

PRIOR FILING DATE: 2000-01-27

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549.50
59.38%
40.23%
36.34%
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US-10-182-447-4
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Best Local Similarity:
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US-09-945-527-48
Sequence 48, Application US/09945527
Sequence 48, Application US/09945527
Publication No. US20030055588A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
UNRENT FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 65
SOUTHWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                               GlnGlyProValIleArgPheTrpProSerGluLyGTrpAlaPheIleGlyValProTyr 260
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SerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGlu
                       538 TCGGGCCTCTGGTGGACCCTGGTCTGCTGGATCAGTGACCGAGCTTTCTGCGAG
                                                                                              LeuLeuSerSerPheHisPheProTyrLeuHisCysValTrpHisIleLeuIleCysLeu
                                                                                                                          AlaSerTyrLeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGlu
                                                                                                                                                                                                                                           658 GCTGCCTACCTGGGTGTATGCTTTGCCTACTTTGATGCTGCCTCAGAGATTCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetGlyAlaProHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys
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                                                                                                                                                                                                                                                                                                                                                                                                                               778 GIGICCCICCIGIGIGCCAACAAGAAATCATCAGICAAGACCACG 822
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Matches:
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Mismatches:
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Gaps:
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665.00
94.74%
91.73%
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US-09-945-527-48
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Query Match:
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Pred. No.:
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Sequence 107211, Application US/10425115
Fublication No. US2004021427241
Fublication No. US2004021427241
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Fublication No. US2004021427241
Fublication No. US2004021427241
Fublication No. US2004021427241
Fublication No. US200404
Fublicant: Kovalic, David K.
FAPPLICANT: Kovalic, David K.
FAPPLICANT: APPLICANTON: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53222) B
FUBLICATION NUMBER: US/10/425,115
FUBLICATION DATE: 2003-04-28
FUBLICATION NUMBER: US/10/107211
FUBLICATION NUMBER: US/10/107211
FUBLICATION 107231
                                                624 ACCTCTGCTGGCTGGTTGATCGCGTCTTCTGCAAGAAGCTTTCGCATGGTACGTCAAC 683
                                                                                                                                                                                                                                                                                                                                                                                                                              684 CCGCAGGGGCACGCGTGGTGGCACGTGCTTATGGCCTCCAACTCGTACTACTACTACACG 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 GTÄCATTTCTTTGCCCGGTTCCAAGTCGTATTC-------AAGCTGCATTAC 512
                                                                                                                                                                        149 IleSerLeuMetIleLeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeuLysArg 168
                                                                                                                                                                                                                                                    169 CysAspAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTrpThrLeuAla 188
                                                                                                                                                                                                                                                                          573 GTGGGTGCGAAGCGGCTCGCAAACTGTGGGTC------CTTACACTGACCCTTGGG 623
                                                                                                                                                                                                                                                                                                                              189 LeuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPhe--- 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 CysPheAlaTyrPheAspAlaAlaSerGluIleProGluGlnGlyProValIleArgPhe 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 TrpProSerGluLysTrpAlaPhelleGly---ValProTyrValSerLeuLeuCysAla 266
                                                                                                                                                                                                              ProTyrLeuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysVal 227
                                                                                            ValCysValLeuSerAlaIleThrThrCysLeuAlaPheIleLysProAlaIleAsnAsn
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                    109 PheProArgArgTyrLeuProLysllePheArgAsnAspArgGlyArgPheLysAlaVal
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121
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Matches:
Conservative:
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220.50
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14.58%
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Query Match:
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/425,114
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                      548
                                                      aleuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPhePr 208
                                                                                                                                  oTyrLeuHisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCy 228
                                                                                                                                                        609 CTATCTGCACAGCATCTGGCATGTGCTCATCACCATCCCTTATGGCATGGTCAC 668
                                                                                                                                                                                                                                                    728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 AATGCTTTCTGCCAAGGTTTTGAAAACGATTTAGTGTCCTGCACATATCCAATATGATA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 ArgGlnTyrAlaThrCysPheAsnSerGlyIleTyrLeulleTrpThrLeuLeuValVal 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
GACCAGGAATAAGGAGCTTCGGCACTGATTGAGGTCTCCGTGGTTTTATGGGCTGTTGC
                                                                                ||||||||
TCTGACCAGCTGGATCAGTGACCGTCTGCTTTGCAGCTTCTGGCAGAGGATTCATTTCTT
                                                                                                                                                                                                              sPheAlaTyrPheAspAlaAlaSerGluIleProGluGlnGlyProValIleArgPheTr
                                                                                                                                                                                                                                14 SerSerGluValAspTrpCysGluAspAsnTyrThrIleValProAlaIleAlaGluPhe
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                                                                                                                                                                                                                                                                                      pProSerGluLysTrpAlaPheIleGlyValProTyrValSerLeu 263
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Mismatches:
Indels:
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US-10-425-114-32295
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Matches:
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Sequence 32295, Application US/10425114

) Publication No. US20040034888A1

GENERAL INFORMATION:
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220.50
43.73$
28.90$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Zea mays
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1270 GGGTGGGGAGCCGCGGATCACACACCTTGGATTCTTGCCTTACGTCAAGGTCCAGAAA 1329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 PheTrpProSerGluLysTrpAlaPheIleGly---ValProTyrValSerLeuLeuCys 265
                                                                                                                                                                                                                  SerSerGluValAspTrpCysGluAspAsnTyrThrIleValProAlaIleAlaGluPhe
                                                                                                                                                                                                                                                                                                                     TACAATACCATCTCTAATGTCCCATGCGTTCTTTTGGCGGTTATTGGATTAGTGAATGCT
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TTCCGCCAA-----GGTTTTGAGAACGGTTCAGTGTCCTTCACGTATCCAATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 AlaLeuPheCysTrpIleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPhe
                                                                                                                                                                                                                                                     513 ACGICAACGACTGAGTTGTGCGAGGAGATTATGCACACTCATCATATATCGCAGAATTC
                                                                                                                                                                                                                                                                                         TyrAsnThrIleSerAsnValLeuPhePheIleLeuProProIleCysMetCys---Leu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1006 TACATTGTCCTGTGCTTCCTCTGCATCCCCCGGATGTACAAGTACTACATACTGACGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 ArgCysAspAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTrpTrpThrLeu
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                                                                                                                                                                                                                                                                                                                                                             PheArgGlnTyrAlaThrCysPheAsnSerGlyIleTyrLeuIleTrpThrLeuLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                    73 ValValGly1leGlySerValTyrPheHisAlaThrLeuSerPheLeuGlyGlnMetLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     904 TGGCACTACAGGAGCACAATGCCA---ACTTTCCTTTTCCTATATGGTGCTGCCTTTGCA
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Conservative:
Mismatches:
Indels:
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                                                      Length:
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US-10-437-963-42300
Sequence 42300, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                      2.31e-13
                                                                   213.50
43.56%
29.92%
14.12%
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                                                                                      Percent Similarity:
Best Local Similarity:
JS-10-767-701-12261
                                     Scores:
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Pred. No.:
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Sequence 12261, Application US/10767701

GENERAL INFORMATION:
APPLICANT: Covalic, David K.
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
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APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Notes: Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (515355) B
CURRENT FILING DATE: 2004-01-29
KUMBER OF SEQ ID NOS: 63128
SEQ ID NO 12261
LENGTH: 1547
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                                                                                                                                                                                                                                                                                                                                        CACTACAGAGCACAATGCCA---ACTITICCTGTTCCTGTATGGTGCTGCCTTTGCCGTA 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 TrpProSerGluLysTrpAlaPhelleGly---ValProTyrValSerLeuLeuCysAla 266
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                                                                                                                                                                                  GIACATTTCTTTGCCCGGTTCCAAGTCGTATTC------AAGCTGCATTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 699 GIIGGCCIICIGCTIGCTCTGCAICCCCCGGAIGIACAAGIACIACAIACAGACGAAAGAC
                TyrAsnThrIleSerAsnValLeuPhePheIleLeuProProIleCysMetCysLeuPhe
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                                                                                                                                                             ValGly1leGlySerValTyrPheHisAlaThrLeuSerPheLeuGlyGlnMetLeuAsp
                                                                                                                                                                                                                                                                                                        109 PheProArgArgTyrLeuProLysIlePheArgAsnAspArgGlyArgPheLysAlaVal
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                                                                                      ArgGlnTyrAlaThrCysPheAsnSerGlyIleTyrLeuIleTrpThrLeuLeuValVal
                                                                                                                                                                                                                                   GluLeuAlalleLeuTrpValLeuMetCysAlaLeuAlaMet----
                                                363 TACAATACCATCTCTAATGTCCCATGCGTTCTTTTGGCACTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
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US-10-767-701-12261
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334 AAGATCAAGAACTCAGTAAACTACCATCTGCTTTTTACCTTAGTTCTATTCAGTTTAATA 393
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                                                   224 LeuGlyCysValCysPheAlaTyrPheAspAlaAlaSerGluIleProGluGlnGlyPro
::::: TGGTACGTCAACCCACAAGGGCACGCATGGTGGCATTTCTCATGGGATTTAACTCATAC
                                                                                                                         244 ValileArgPheTrp---ProSerGluLysTrpAlaPheIleGlyValProTyrValSer
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                                                                                      TTTGCAAACACA - - TTCTTAATGTTTTGCCGAGCTCAACAG
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                              Sequence 5, Application US/10182447
Sequence 5, Application US/10182447
Fublication No. US20030185814A1
GENERAL INFORMATION:
APPLICANT: HOFMANN, KAY
TITLE OF INVENTION: CERAMIDASE
FILE REFERENCE: P68055USO
CURRENT APPLICATION NUMBER: US/10/182,447
CURRENT FILING DATE: 2002-07-29
FRIOR APPLICATION NUMBER: PCT/EP01/0090
FRIOR FILING DATE: 2001-01-27
FRIOR FILING DATE: 2000-01-27
FRIOR FILING DATE: 2000-01-27
FRIOR APPLICATION NUMBER: DE 10011392.3
FRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 5
SEQ ID NO 5
                                                                                                                                                                                                                    968 ATTCAGAAACCCCAAAAGAGG 988
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209.50
40.89%
30.11%
13.86%
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Best Local Similarity:
Query Match:
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                                                 APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Buckharv, Andrey A.
APPLICANT: Barbazuk, Barad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnMetLeuAspGluLeuAlaIleLeuTrpValLeuMetCysAlaLeuAlaMet---- 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :::::: ::: ||| :::||| :::||| ---TTGCATTACATTACGTTACATA 703
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Matches:
Conservative:
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Indels:
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212.50
42.70%
27.34%
14.05%
 La Rosa, Thomas J
Kovalic, David K
Zhou, Yihua
Cao, Yongwei
                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Oryza sativa
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Best Local Similarity:
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LENGTH: 1436
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Rovalic, David K.
APPLICANT: APPLICANT: About Yihua
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yihua
APPLICANT: Pants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 77897
LENGTH: 1429
                44 ACCTCCACGCTGGACTGGTGCGAGAGAACTACTCCGTGACCTGGTACATCGCCGAGTTC 103
                                                                                             104 IGGAATACAGIGAGIAAC---CIGAICAIGATIAIACCICCAA--IGIICGGIGCAAIIC 158
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US-10-425-115-77897
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, Y. Tom

APPLICANT: Tang, Y. Tom

APPLICANT: Drmansc., Radoig J.

APPLICANT: Drmansc., Radoig T.

APPLICANT: Drmansc., Radoig T.

APPLICANT: Drmansc., Radoig T.

APPLICANT: Drmansc., Radoig T.

APPLICANT: Drmansc., Radoig T.

APPLICANT: NUMBER: US/10/302,172

CURRENT APPLICATION NUMBER: US 10/225,251

PRIOR PILING DATE: 2002-08-20

PRIOR PILING DATE: 2002-08-20

PRIOR PILING DATE: 2002-08-30

PRIOR PILING DATE: 2001-03-05

PRIOR PILING DATE: 2001-03-05

PRIOR FILING DATE: 2001-03-05

PRIOR FILING DATE: 2001-03-05

PRIOR FILING DATE: 2001-03-05

ANUMBER OF SEQ ID NOS: 950

SOFTWARE: DL. Genes Version 2.0

SOFTWARE: DL.

CREBGIT: 1063

TYPE: DNA

ORGANICM: Homo sapiens
      AlalleThrThrCysLeuAlaPhelleLysProAlalleAsnAsnIleSerLeuMetlle 153
                                     GTAACCACAGTTTACCTTAAGGTAAAAGAGCCAATATTCCATCAGGTCATGTATGGAATG 453
                                                                       LeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeuLysArgCysAspAsnValArg 173
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Matches:
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CTTTTCAGTTTGTAT------
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Best Local Similarity:
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; LOCATION: (2)
US-10-302-172-875
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    Sequence 2429, Application US/10017161

Publication No. US20030143668A1

JGBURRAL INFORMATION:
APPLICANT: SUNA, MAKIKO
APPLICANT: AKIYAMA, YUTAKA

TILLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS

TILLE OF INVENTION NOVEL G PROTEIN-COUPLED
CURRENT APPLICATION NUMBER: US/10/017,161

CURRENT FILING DATE: 2002-12-18

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEQ ID NOS: 2430

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 2429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-017-410-2 (1-275) x US-10-017-161-2429 (1-35425)
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (35270)...(35425); OTHER INFORMATION: a, t, c, g, unknown or other US-10-017-161-2429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
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LOCATION: (35125)..(35225)
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LOCATION: (21462)..(21603)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (26868) .. (27016)
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                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (201)..(293)
FEATURE:
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LOCATION: (1)..(35425)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      937 TTAACCCTTGGGACTCTCTGCTGGCTGGTTGATCGCATTTTTTGCAAAAAGCTTTTGCAT 996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 ValileArgPheTrpProSerGluLysTrpAlaPheileGly---ValProTyrValSer 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                 724 regecegacióscarracaddageacacaargéca---accircerrrecrarardodger 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlubeulysArgCysAspAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTrp 184
                                                                                                                                                                                                                                                                 502 TACAACAACAATTTCTAATGTC-------CCATGTGTTCTTTTGGCGCTT 543
                                                                                                                                                                                                                                                                                                                                                                                    34 TyrAsnThrileSerAsnValLeuPhePheIleLeuProProIleCysMetCysLeuPhe 53
                                                                                                                                                                                                                                                                                                                                                                   54 ArgGlnTyrAlaThrCysPheAsnSerGlyIleTyrLeuIleTrpThrLeuLeu---- 71
                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ValValValGlyIleGlySerValTyrPheHisAlaThrLeuSerPheLeuGly
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Matches:
Conservative:
Mismatches:
Indels:
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; TYPE: DNA
) ORGANISM: Zea mays
; PRATURE:
) OTHER INFORMATION: Clone ID: MRT4577_171065C.1
US-10-425-115-77897
                                                                                                   1.23e-12
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Best Local Similarity:
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1150 GTC 1152
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BW351328

Total number

BW216493

AMGNINUC: N Salamande Salamande 170006870

AL864302

OM protein

Run on:

Sequence: Title: Perfect :

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. 1 (bases 1 to 1022)

E. 1 (bases 1 to 1022)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. David Rowe

CDNA Library Preparation: Invitrogen Corp

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLANHAG7 row: j column: 05

High quality sequence stop: 681.
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BY168309
BJ062108
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CB784796 I
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CA969385
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BU511164.1 GI:22817397
EST
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/clone="IMAGE:6505924"
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BW215750
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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 SOURCE
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-Q=/Cogn2 1/USPTFO spool p/USIO17410/runat 19112004 133620 19010/app_query.fasta_1.455
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AGENCOURT
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3355.970 Million cell updates/sec
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                                                                                                                                                                                                  US-10-017-410-2
1512
1 MGAPHWWDHIRAGSSEVDWC.....IGVPYVSLLCAHKKSPVKIT 275
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CA976684 A
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                       using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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CA976684
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AY401889
AF370405
BU234223
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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gb_btc::*;
gb_est3::*
gb_est6:::*;
gb_gss1::*;
gb_gss1::*;
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Mus musculus HCM1041 gene, VIRTUAL TRANSCRIPT, partial sequence, AY401891
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Rerriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 MetCysLeuPheArgGlnTyrAlaThrCysPheAsnSerGlyIleTyrLeuIleTrpThr
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     900 CCTATGGGTCCCTTCTGTGTGCCCAACAGAAGTCGCCAGTCAAGATC
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Science 302 (5652), 1960-1963 (2003)
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/db_xref="taxon:10090"
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Mus musculus
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AUTHORS
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KEYWORDS
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/tissue type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC 114"
/note="wetcor: PGWV-SPORT6.1; Site 1: EcoRV; Site_2: NotI;
/lone unidirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
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	170 AspAsnValArgValPheLysLeuGlyLeuPheSerGlyLeuTrpTrpTrpThrLeuAlaLeu 189	361 GACAAIGIGGIGIGITITAAGCIGGGCCICTICICIGGGCICTGGGGGGCTCTGGCTCTC 420	190 PheCysTrplleSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPheProTyr 209	421 TICTGCTGGATCAGCGACCAAGCCTTCTGTGAGCTGCTCTTCTTTCACTTCCCCTAC 480	210 LeuhisCysValTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCysPhe 229	481 CTGCACTGTGTGTGTGTTTTTTTTTTTTTTTTTTTTTTT	230 AlaTyrPheAspAlaAlaSerGluIleProGluGlnGlyProVallleArgPheTrpPro 249	541 GCCTACTTTGATGCTGCCTCAGAGATACCTGAGCAAGGTCCAGTCATCAGATTCTGGCCC 600	250 SerGluLysTrpAlaPhelleGlyValProTyrValSerLeuLeuCysAlaHisLysLys 269	601 AGGAGAAAIGGGCTITIAIIGGIGICCTIAIGIGICCTICTGIGIGCCCACAAGAAG 660	270 SerProValLysileThr 275	661 TCGCCAGTCAAGATCACG 678		CA976684 8677974 NCI_CGAP_Mam2 Mus musculus cDNA clone	IMAGE:6437893 5', mRNA sequence. CA976684 CA976884 I GT:27509338	EST. (Lease of the control of the co	Mus musculus (nouse mouse) Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Murinae; Mus.	1 (bases 1 to 868) NIH-MGC http://mgc.ncj.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	Onpublished (1999) Contact: Robert Strausberg, Ph.D.	Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith. Ph.D.	CDNA Library Preparation: Life Technologies, Inc.		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	http://image.llnl.gov Plate: LLAM13955 row: g column: 14	High quality sequence stop: 679.		/organizem="muse museculus" /mol_type="mRNA" /etyaia_mermonal"	/brain= Fvb/w-3 /db ref=fraon:10090" /al == ref=fraon:10090"	/clone='lmwks.bd3's" /tissue_type="tumor, biopsy sample"	/dev_stage="5 months" /lab_host="DH10B"	/clone_lib="NCI_CGAP_Mam2" /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;	<pre>ble=z: NOC1; Cloned unldirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith. NTH"</pre>	
Ωp	λŏ	qa	λŏ	qu	ζ	qu	, vo	qa	, vo			og o	RESULT 3 CA976684	LOCUS	ACCESSION	KEYWORDS	SOURCE		REFERENCE AUTHORS	TITLE	COMMENT						FEATTIRES	sonice							ORIGIN

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Length:

6.5e-111

Alignment Scores: Pred. No.:

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AK085306
Mus musculus 0 day neonate Kidney DNA, RIKEN full-length enriched library, clone:D630008P07 product:similar to CANCER RELATED GENE-LIVER 1 [Mus musculus], full insert sequence.
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AKO85306.1 GI:26351558
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
99279253
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GILVAELKRCDNVRVFKLGLFSGLWWTLALFCWISDQAFCELLSSFHFPYLHCVWSADR
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Pan troglodytes HCM1041 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
AY401890.1 GI:39757876
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I. Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboration Research Group, RIKEN Genome Center (GSC), RIKEN Yokohama Institute; 1.7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, UKL: http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
   Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
10499374
                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watsuhiki, M., Ohaca, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1173)
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similar to CANCER RELATED GENE-LIVER 1 [Mus musculus]
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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/organism="Mus musculus"
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100 371 120 431 140 491 160 551 180 611

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229 540 249 009 EST 12-NOV-2002

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5'-ATTCTAGAGGCCGAGGCGGCAATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5 kb size fraction. Library created in thelaboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
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Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 797)
1 (hases 1 to 797)
1 National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
TICTGCTGGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCAACTTCCCCTAC 480
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Plate: LLCM3088 row: p column: 08
High quality sequence stop: 536.
Location/Qualifiers
                                                   LeuhisCysValTrphisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCysPhe
                                                                                 AlaTyrPheAspAlaAlaSerGluIleProGluGlnGlyProValIleArgPheTrpPro
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
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                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan. (base, 1 to 681)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perirera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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/mol_type="genomic DNA"
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Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M. Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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Matches:
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Mismatches:
Indels:
 Science 302 (5652), 1960-1963 (2003)
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/db_xref="taxon:9606"
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1 (bases 1 to 681)
1 (Alanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adans, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
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                                  MetGlyAlaProHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.

Phasianinae; Gallus.

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

Curr. Biol. 12 (22), 1965-1969 (2002)
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gallus cDNA clone ChEST757k21 5', mRNA
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                                                 ACGTGCCTGGCATTTGTCAAGCCTGCCATCAAAAACATCTCTCTGATGACCCTGGGAGTT
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ELAVLWVLMCALAMWFPRRYLPKIFRNDRGRFKVVVSVLSAVTTCLAFVKPAINNISL
MTLGVPCTALLIAELKRHERNQRRRHRKGGQQGGGDKV"
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Huang, Y., Zhou, X.M., Zhang, P.P., Jiang, H.Q., Qin, W.X., Zhao, X.T., Wan, D.F. and Gu, J.R.
Novel human cDNA clones with function of inhibiting cancer cell
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Submitted (16-APR-2001) National Laboratory For Oncogenes (Genes, Shanghai Cancer Institute, 25/Ln 2200 Xie-Tu Road, 200032, P. R. China
Location/Qualifiers
1. 1527
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Zhang, P.P., Zhou, X.M., Jiang, H.Q., Huang, Y., Qin, W.X.,
Wan, D.F. and Gu, J.R.
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Conservative:
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Homo sapiens PP11646 mRNA, complete cds.
AF370405
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/codon_start=1
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Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V., Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B., Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B., Plopper,C.G. and Buckpit,A.M. response to lung toxicants: I. Sequencing and microarray development.

Squencing and microarray development.

Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)

Contact: Shultz MA

Dept. of Molecular Biosciences, School of Veterinary Medicine University of California, Davis

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Tel: 530 752 0933

Fax: 530 752 4698

Email: mashultz@ucdavis.edu

Average Phred score is 20 or better. All poor quality data (Phred < 20) and vector/linker sequence has been removed.

High quality sequence stope: 565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF115220 555 bp mRNA linear EST 23-JUL-2003
Shultzomica08471 Rat lung airway and parenchyma cDNA libraries
Rattus norvegicus cDNA clone NP6159 5', mRNA sequence.
CF115220
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/dev_stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/clone_lib="Organ: lung; Vector: pGEM-112f(-); Site_1: Eco RI;
Site_2: Not I: mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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/organism="Rattus norvegicus"
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="NP6159"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysllePheArgAsnAspArgGlyArgPheLysAlaValValCysValLeuSerAlaIle 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTACCTGCCTTGCTTCATTAAACCTGCCATCAACATCTCACTAAIGACTCTGGGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysLeuGlyLeuPheSerGlyLeuTrpTrpThrLeuAlaLeuPheCysTrpIleSerAsp 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTATTCTCTGGGTCCTTATGTGTGCTCTTGCCATGTGGTTCCCTAGGAGATATCTACCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AGAGTTTTTCGAAATGACAGGAGCCGGTTTAAAGCTGCTGTTGGTGTCCTGTCTGGAGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thr Thr Cysteu Ala Phelle Lys Pro Alalle Asn Asn Ile Ser Leu Met Ile Leu Gly 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuProCysThrAlaLeuLeuValAlaGluLeuLysArgCysAspAsnValArgValPhe 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGCTTGGTCTGTTTTCAGGTCTTTGGTGGATGCTAGCACTTTTTCTGCTGGATCAGTGAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnAlaPheCysGluLeuLeuSerSerPheHisPheProTyrLeuHisCysValTrpHis 215
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                                                                                                               of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                            1. .698
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST757k21"
                          Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of
(UMIST)
PO Box 89, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
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81 PheHisAlaThrLeuSerPheLeuGlyGlnMetLeuAspGluLeuAlaIleLeuTrpVal 100
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RS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Haraka,A., Hiramaco,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Salto,R., Shiraki,T., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTS (Arakawa,T., et al. 2001)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eSerAspGlnAlaPheCysGluLeuLeuSerSerPheHisPheProTyrLeuHisCysVa 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 lTrpHisIleLeuIleCysLeuAlaSerTyrLeuGlyCysValCysPheAlaTyrPheAs 233
                                                                                                                                                                                                   133 rAlalleThrThrCysLeuAlaPheIleLysProAlaileAsnAsnIleSerLeuMetil 153
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Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
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                                                                                                                                                                                                                                                                                                                                                      TCTGGGGGTTCCGTGCACTGCTGCTCATTGCAGAGCTGAAGAGGTGTGACAATGTGG
                                                                                                                                                                                                                                   rLeuProLysIlePheArgAsnAspArgGlyArgPheLysAlaValValCysValLeuSe
BB660847 BIKEN full-length enriched, 0 day neonate kidney Musmusculus cDNA clone D630008P07 5', mRNA sequence.
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/note="Site 1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was primed with a primer [5].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fyukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
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                                                                                                                                                                                                                                                                                                                                     Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/lone lib="RIKEN full-length enriched, 0 day neonate
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633 185 0 3 Conservative: Mismatches: Matches: Length: Indels: 1.85e-91 986.00 97.88**%** 97.88**%** 65.21**%**

US-10-017-410-2 (1-275) x BB660847 (1-633)

	hrileSerAsnVal 40	yrAlaThrCysPhe 60	leglyServalTyr 80
	CGATCAGCAACGTC 188	ACGCAACGTGCTTC 248	TTGGATCTGTCTAC 308
1 MetGlyalaProHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys 20	21 GluAspAsnTyrThrIleValProAlaileAlaGluPheTyrAsnThrIleSerAsnVal 40 	41 LeuphepheileLeuproproileCysMetCysLeubheArgGlnTyrAlaThrCysPhe 60	61 AsnSerGlylleTyrLeulleTrpThrLeuLeuValValValGlylleGlySerValTyr 80
1 M	21 G	41 L	61 A
— A	129 G		249 A
S	Qy	oy	oo qa
S	Db	ag	

Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."	Alignment Scores: 2.9e-91 Length: 622 Pred. No.: 5622 Score: 180 Percent Similarity: 78.95\$ Conservative: 0 Best Local Similarity: 78.95\$ Mismatches: 2	Gaps: Gaps: 138 (1-622)	Qy 1 MetGlyAlaProHisTrpTrpAspHisLeuArgAlaGlySerSerGluValAspTrpCys 20	Qy 21 GluAspAsnTyrThr11eValProAlaileAlaGluPheTyrAsnThr11eSerAsnVal 40	Qy 41 LeuPhePheIleLeuProProIleCy8MetCy8LeuPheArgGlnTyrAlaThrCy8Phe 60	Oy 61 ABRSERGIVILETVILEUIETRITHILIEULEUVAIVAIVAIGIVILEGIVSERVAITYR 80	Qy 81 PheHisAlaThrLeuSerPheLeuGlyGlnMetLeuAspGluLeuAlaIleLeuTrpVal 100	Qy 101 LeuMetCyBAlaLeuAlaMetTrpPheProArgArgTyrLeuProLyBIlePheArgAsn 120	AspArgGlyArgPheLysAlaValValCysValLeuSerAlaIleThrThrCysLeuAla	Db 436 GAC 438 Qy 141 PhelleLysProAlalleAsnAsnIleSerLeuMetIleLeuGlyLeuProCysThrAla 160	438	Oy 161 LeuleuvalataGilleeurgesteryeAsbaantairegusterieleurgesterie	Oy 181 SerGlyLeuTrpThrLeuAlaLeuPheCysTrpIleSerAspGlnAlaPheCysGlu 200	201 LeuLeuSerSerPheHisPheProTyrLeuHisCysValTrpHisIleLeuIleCysLeu	n	Db 598 GCTTCGTACTGGGCTGTCG 621	RESULT 13 BU232554 LOCUS BU232554 T81 bp mRNA linear EST 26-NOV-2002 DEFINITION 603409105F1 CSEQCHN24 Gallus gallus cDNA clone ChEST323j2 5', mRNA	ACCESSION BU232554.1 GI:25475352 KEYWORDS EST GAllus GAllus (chicken)	NISM Gallus gallus Eukaryota; Met
Db 309 TTCCATGCAACGCTGAGTTTCCTGGGTCAGATGCTTGATGAACATGCCATTCTGTGGGTT 368 Oy 101 LeuMetCysalaLeuAlaMetTrpPheProArgArgTyrLeuProLysillePheArgAsn 120	Db 369 CTGATGTGTGTTTTGGCCATGTGTTTTCCAGAGGTTTTTTTT	Qy 141 PhelleLysProAlaileAsnAsnileSerLeuMetIleLeuGlyLeuProCysThrAla 160	Qy 161 LeuleuValAlaGluLeuLysArgCysAspAsnValArgValPheLysLeuGly-LeuPh 180	Qy 180 eSerGlyLeuTrpThrLeuAla 188 bb 609 TTTGGCCTTGTGGTGGACTCTGGCT 633	RESULT 12 CB723138 LOCUS CB723138 622 bp mRNA linear EST 09-JUL-2003 DRENITORN III-M-CHD-ceh-f-04-0-III 21 NTH RMAD CHO Mag macanjas Chone	IMAGE:6839525 5', mRNA sequence. CB723138 CB723138.1 GI:29780280	EST. Mus musculus (house mouse) 1 Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostc	Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. REFERENCE I (bases I to 622) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC)	JOUKNAL Unpublished (199) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov	Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa			FEATURES LOCATION/QUALITIEFS 1622 /organism="Mus musculus" /mol tyne="MRNA"	<pre>/strain="C57BL/6" /db_xref="taxon:10090" /clone="IMAGE:6839525" /clone="IMAGE:6839525"</pre>	/t188ug-fype="#Mole brain" /dev stage="1"5, and 15 days newborn" /lab_host="DH10B (T1 phage resistant)"	/clone lib="NIH BMAP GHO" /note="Organ: Brain; Vector: pXx- Asc; Site 1: BcoR I; cite 2. Not I. The library was constructed according	Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand CDNA synthesis was primed with oligo-dr primer containing a Not I site. Double strand cDNA was	size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not1 and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAACHGAAT. This library was created for the Injuversity.	Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National

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CF169369 S48 bp mRNA linear EST 25-JUL-2003 B0812G07-5 NIA Mouse Newborn Kidney cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0812G07 IMAGE:30468654 5', mRNA sequence.
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Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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                          spGlnAlaPheCysGluLeuLeuSerSerPheHisPheProTyrLeuHisCysValTrpH
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
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ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand reaction. double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-923 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                             Bosch, E.,
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                   Phasianinae; Gallus.

1 (bases 1 to 781)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 IleGlySerValTyrPheHis-AlaThrLeuSerPheLeuGlyGlnMetLeuAspGluLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uAlaileLeuTrpValLeuMetCyBAlaLeuAlaMetTrpPheProArgArgTyrLeuPr
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                                                                                                                                                                                                         Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
Tel: 01612008930
Fax: 01612360409
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    781
177
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                 organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                    Bmail: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-017-410-2 (1-275) x BU232554 (1-781)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9031"
/clone="ChEST323j2"
                                                                                                                                                                  12445392
Contact: Simon Hubbard
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Query Match:
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JOURNAL
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                                                             AUTHORS
                                         REFERENCE
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purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centrion 100. Then, the CDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Sal1 and Not1 enzymes and cloned into Sal1/Not1 site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValValCysValLeuSerAlaileThrThrCysLeuAlaPheileLysProAlaileAsn 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABILESErLeuMetILELeuGlyLeuProCysThrAlaLeuLeuValAlaGluLeuLyg 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 15

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BJ060795 BJ060795 NIBB Mochii normalized Xenopus tailbud library Xenopus laevis cDNA clone XL066n16 5', mRNA sequence.
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                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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/db xref="taxon:835s"
/clone="XL066n16"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
libxary"
                                                                                                                                                                                                                                                                                                                                                                     Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T.
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162
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressed genes in X. laevis embryo Unpublished (2001)
Contact: Tadaeu Shin-i Center For Genetic Resource Information National Institute of Genetics
Ill Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone
URL.
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        GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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•	* Query	Match	98.1	98.1	92.7	91.9	80.3	50.4	38.0	37.3	37.3	29.0	28.8	26.2	22.7	22.7	22.2	22.1	21.4	18.6	18.6
		Score	812	812	767.6	191	664.8	417.2	315	308.6	308.6	239.8	238.2	216.6	188	188	183.6	183.4	177.2	154.4	154.4
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construction: Helix Research Institute (HRI) (supported by Japan Rey Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation, clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers

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/note="cloning vector: pME185FL3"
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larity 98.8%;
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Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamateu,A., Ishii,S.,
Yamamotco,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Wateuo,K., Nakamura,Y., Sekine,M.,
Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K.,
Takahashi-Fulii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
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Isogai, T. and Yamamoto, J.
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDo human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; CDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
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AK123581.
Gligo capping; fis (full insert sequence).
Homo sapiens (human)
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VECTOR: PRACE3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-310K15, 2000 bp overlap;
the clone sequenced to the right is RP11-156A1, 2000 bp overlap;
the clone sequenced to the right is RP11-156A1, 2000 bp overlap.
Actual start of this clone is at base position 190775 of
RP11-310K15; actual end is at base position 28935 of RP11-156A1.

(http://bacpac.med.buffalo.edu)

The sequence between 81601 and 81703 is covered only by a pcr product of clone DNA. Unresolved tandem repeat regions exist between 81548 and 83183, 126196 and 127426.
Location/Qualifiers

. .149462

FEATURES

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Submitted (09-JAM-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jan 9, 2002 this sequence version replaced gi:14165368.
                                                                                                                      PRI 09-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
4 (Dases 1 to 149462)
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1 (Dases 1 to 149462)
Sulston, J.E. and Waterston, R.
                                                                                                                    AC017081 149462 bp DNA linear PRI 09-07
Homo gapiens BAC clone RP11-470424 from 2, complete sequence
2 (bases 1 to 149462)
Nguyen, C., Doebber, A. and Kozlowicz, A.
The sequence of Homo sapiens BAC clone RP11-470J24
Unpublished (2001)
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Genome Res. 8 (11), 1097-1108 (1998)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Center: Washington University Genome Sequencing Center

Genome Center

Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu

Center code: WUGSC

Center project name: H_NH0470J24

Louis Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. I. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc MAPPING INFORMATION:

restriction digest.

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute

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CAAGGCCCTGTCATCAAATTCTGGCCCAGCGAGAAATGGGCCTTCATTGGTGTCCCCTAT 136144
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                           CTGATGTGTGCTTCGGTCATGTGGTTCCCCAGAAGGTATCTACCAAAGATCTTTCGGAAT
                                                                                                                                   TTCCATGCAACCCTTAGTTTCCTGGGTCAGATGCTTGATGATGAACTTGCAGTCCTTTGGGTT
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                                                          AACAGTGACATCTACTTAATCTGGACTCTTTTGGTTGTAGTGGGAATTGGATCCGTCTAC
                                                                                                                  TICCATITITACCCTITAGITICTIGGGICAGAIGCTIGAIGAACITGCAGICCTTIGGGGIT
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Patent: WO 0155408-A 6 02-AUG-2001;
Memorec Medical Molecular Research Cologne Stoffel GmbH (DE)
Location/Qualifiers
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AX206799
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10320. 10341
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9378. .9422
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13139. .16061
/rpt family="Li"
16063. .17107
/rpt family="Li"
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8177. .18501
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LLVAELKRCDNVRVFKLGLFSGLWWTLALFCWISDQAFCELLSSFHFPYLHCVWHILI
CLASYLGCVCFAYFDAASEIPEQGFVIRFWPSEKWAFIGVPYVSLLCAHKKSPVKIT"
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                                                                                         2 (bases 1 to 4174)
Garveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
Identification of genes deregulated in murine hepatocellular
carcinomas using oligonucleotide microarrays and representational
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Pred. No. 1.1e-169;
0; Mismatches 102; Indels
     novel
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   profiling and identification of
                      hepatocellular carcinomas
Oncogene 20 (21), 2704-2712 (2001)
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Earnham, D.J. and Graveel, C.R.
Direct Submission
Submitted (27-JUN-2000) Oncology,
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'product="cancer related
                                                                                                                                                                                                                                                                                                                                                                                                                       'note="CRG-L1; putative'
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Unpublished
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Graveel, C.R., Jatkoe, T., Madore, S.J., Holt, A.L. and Farnham, P.J.
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tribution: MGC clone distribution information can be found the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov RAK plate: 132 Row: o Column: 4 le was selected for full length sequencing because it is following selection criteria: matched mRNA gi: 21314857. Location/Qualifiers
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HGCTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAAGATCTTTCGGAAT ricertrigeccarerectricecaegaearriraccaaagarerreegaar

435

STAGGTTCAAGGTGGTGGTCAGTGTCCTGTCTGCGGTTACGACGTGCCTGGCA 420

Oy 694 TTTGATGCTGCCTCAGAGATTCCTGAGGCCCTGTCATCAGGTTCTGGCCCAATGAG 753		NEFERENCE 1 AUTHORS Venter, C., Adams, M.C., Li, P.W. and Myers, E.W. TITLE Xits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof JOURNAL Patent; WO 02068579-A 22839 06-SEP-2002; PE Corporation (NY) (118)	FEATURES Location/Qualifiers 1. 315 315	Query Match 37.3%; Score 308.6; DB 6; Length 315; Best Local Similarity 98.7%; Pred. No. 8.4e-73; Matches 311; Conservative 0; Mismatches 4; Indels 0; Gaps 0; QY 514 AngcongraphanderGaggectrtTcTcGagaccTcTcGGagacCTTTTCTGG GCTTTTTTGGGGCTCTTCTCGGGCCTCTTCTTGGCGACCTTTTTTGCGAGCTCTTCTTGGGGCTCTTTTTTGCGAGCTTTTTTGCGGGCTCTTCTTGGCGCTTTTTTGCGGGCTCTTTTTT	Db 61 TGGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCAACTTCCCCTACCTGCAC 120 Qy 634 TGCATGTGGCACATCCTCTGCTGCTGCTGCTGTGTATGCTTTGCCTAC 693 Db 121 TGCATGTGGCACATCCTCATCTGCTGCTTGCTGGCTGTATGCTTTGCCTAC 180 Ov 694 TTTGATGGTGCTGCCTCAGAGATTCCTGAGCAAGGCCTGTCATCAGTTATGCTTTGCCTAC 180	181 TITGATGCCCCCAGAGAITCCTGAGCAGGCCCTGTCATCAAITCTGGCCCAGCGAG 754 AAAIGGGCCTTCATTGGTGTCCCCTATGTGTCCCTGTCATGTGTCCAAAITCTGGCCCAGCGGG 754 AAAIGGGCCTTCATTGGTGTCCCCTATGTGTCCCTCTGTGTGCCAACAAAAATCATCA 814 GTCAAGATCACGTGA 828 814 GTCAAGATCACGTGA 315 301 GTCAAGACCACGTGA 315	RESULT 9 CQ736906 LOCUS LOCUS CQ736906 DEFINITION Sequence 22840 from Patent WO02068579. ACCESSION CQ736906 VERSION CQ736906.1 GI:42333767
	Db 478 ICIGGCCTCTGGTGACTCTCTCTGCTGGATCAGCGACCAAGCCTTCTGTGGG 537 Qy 601 CTGCTGTCATCCTTCAACTTCCCCTACCTGCACTGGGATCAGCGACCAAGCCTTCTGTGGG 537 Qy 601 CTGCTGTCATCCTTCAACTTCCCTACCTGCACTGTGTGGCCAAGCCTTCTGCCTT 660 Db 538 CTGCTTCCTTTCACTTCCCTACCTGCACTGTGTGGCCATATTCTCATCTGCCTT 597 Qy 661 GCTGCCTACCTGGGTGTATGCTTTGCCTACTTGATGCTCAGAGATTCCTGAG 720 Db 598 GCTTCTACACTGGGTGTATGCTTTGCCTACTTGATGCTCAGAGATTCCTGAG 720 CTGCTACTACTACTGCTTTGCTTTGCTTACTTTGATGCTTGATGATGATGATGATGATGATGATGATGATGATGATGA	721 CAAGGCCTGTCATCAAGTTCTGGCCCAATGGGAATGGGCCTTCATTGGTGTCCCTAT 721 CAAGGCCCTGTCATCAAGTTCTGGCCCAATGGGACTTCATTGGTGTCCCCTAT 781 GTGCCCTCCTGTGGCCAACAAGAAATGGGCTTTTATTGGTGTCCCTTAT 781 GTGCCCTCCTGTGCCAACAAGAAATCATCAGTCAAGATCACGTGA 828 118 GTGCCCTCCTGTGTGCCAACAAGAAATCACGTGA GAATCAGTGA 765	RESULT 7 CC744096 LOCUS CQ744096 315 bp DNA linear PAT 03-FEB-2004 DREINITION Sequence 30030 from Patent WO02068579.	S ISM CE RS	NAL ES ource	ORIGIN Query Match Best Local Similarity 100.0%; Score 315; DB 6; Length 315; Batches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 514 ANGCONGTOTITAAGCIGGGCCTCTTCTCGGGCCCTCTGGTGGACCCTGTTCTGC 573 Db 1 ANGCONGTOTITAAGCIGGGCCTCTTCTCGGGCCCTCTGGTGGACCCTGTTTCTGC 60 Qy 574 TGGATCAGTGACCGAGCTTTCTCGGGCCTCTTCAGCTGGCCTGCTTCTGC 633	Db 61 TGGATCAGTGACCTTTCTGCGAGCTGCTTTTTTTTTTTT

us-10-017-410-3.rge

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                                                                                                                                                                                       Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berkeley, CA 9472 mustoned as part of a high-throughput process to rhis clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are stifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription et course that result in single base changes. For further information about this sequence, including its location (http://fruitfly.berkeley.edu.) or send email to change it considered that the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant o
                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 2318)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G.,
Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S.,
Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
                                                                  INV 20-DEC-2001
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DELALLWVFMAAFSLFYPKRYYPKFVKNDRKTFSWLMILLSAIAATGLSWWKPIVNAFV
LMFMSVPTWVMLYTELQRVSDQRVYRLGIRSTTVWAVAVFCWINDRIFCEAWSSINFP
YLHGFWHIFIFIAAYTVLVLFAXFYVESELPQRQPLLKYWPKNEFEFGIPFISIRNPG
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                                                                                                                                                                                                                           Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (18-DEC-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley, National Laboratory
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Drosophila melanogaster RE26924 full length cDNA.
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/organism="Drosophila melanogaster"
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Pred. No. 1.5e-53;
0; Mismatches 318;
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|db_xref="GI:17945606"
|db_xref="FLYBASE:FBgn0032842"
                                                                                                                                                                                                    Drosophila melanogaster (fruit fly)
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="38B4-38B5"
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/note="Longest ORF"
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Best Local Similarity 57.4%;
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RESULT 11
AY071232
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TGGGACCAGCTGCAGCTGGTAGCTCGGAGGTGGACTGGTGCGAGGACAACTACACCATC
                                                                                                      GTGCCTGCTATCGCCGAGTTCTACACACACACACACAATGCCAATGTCTTATTTTCATTTTACCCG
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A cDN resource from the basal chordate Ciona intestinalis Genesis 33 (4), 153-154 (2002)
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Ciona intestinalis cDNA, clone:citb013n14, AK116177.1 GI:23588622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 TGTTGGTGCTGGCTCCGTGTATTTTCACTCAACTTTAAGCCTTGTTGGCCAGTTAATTGA 354
              Satou, Y. and Satoh, N.
Direct Submission
Submitted (04-OCT-2002) Nori Satoh, Kyoto University, Department
                                                                                                                                                                                                                                                                                                                                                                                                                             TGAACTTGCAGTCCTTTGGGTTCTGATGTGTGCTTTTGGCCATGTGGTTCCCCAGAAGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 AGTGGGAATTGGATCCGTCTACTTCCATTTTACCCTTAGTTTCTTGGGTCAGATGCTTGA
                                                                Zoology; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan (E-mail:satohoascidian.zool.kyoto-u.ac.jp, Tel:81-75-753-4095, Fax:81-75-705-1113)
Ciona intestinalis CDNA Project (URL: //ghost.zool.kyoto-u.ac.jp/indexr1.html).
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                                                                                                                                                                                                                                                                                           Length 1429;
                                                                                                                                                                                                                                                                                         Score 216.6; DB 3;
Pred. No. 1.1e-47;
0; Mismatches 329;
                                                                                                                                                                                   /organism="Ciona intestinalis"
/mol_type="mkn3"
/db_xref="teaxon:719"
/clone="cibol3n14"
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Direct Submission

Submitted (25-JUN-2000) Sanger Centre, Hinxton, Cambridgeshire, Callo 18A, UK. E-maile nequisities: hunquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

On Jul 7, 2000 this sequence version replaced gi:8651879.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence map criteria as follows. An attempt is made to resolve all sequence map criteria sollows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Bm:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORWDEP; Information on the WORWDEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
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RP11-363E7 is from the library RPCI-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
   PRI 28-JUN-2000
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163542 bp DNA linear PRI 28-JUN-2000 sequence from clone RP11-363E7 on chromosome 9, complete
                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 163542)
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/clone_lib="RPCI-11.2"
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Best Local Similarity 100.
Matches 188; Conservative
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97064 CTGCCTCAGAGATTCCTGAGCAAGGCCCTGTCATCAAGTTCTGGCCCAATGAGAAATGGG 97005
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    ..795
/function="deacylates ceramide to generate sphingosine and

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Mao, C., Xu,R. and Obeid,L.M.
Molecular cloning and characterization of a novel human alkaline
                                                                                                                                                                                                                                                                                                                                                                                               641 GGCACATCCTCATCTGCCTTGCTGCTTGCTGTGTATGCTTTGCCTACTTTGATG
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Mao,C., Xu,R. and Obeid,L.M.
Direct Submission
Submitted (08-FEB-2001) Medicine, Medical University of South
Carolina, 171 Ashley Avenue, Charleston, SC 29425, USA
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0
                                                                                                                                                                                                                                                                                       Length 219679;
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Homo sapiens alkaline ceramidase mRNA, complete cds.
AF347024
                                                                                                                                                                                                                                                                                  22.7%; Score 188; DB 2; Length 21 100.0%; Pred. No. 1e-39; ive 0; Mismatches 0; Indels
                                                                                                                                             /chromosome="5"
/clone="RP11-170C8"
/clone_lib="RPCI human BAC library 11"
                                                                  organism="Homo sapiens"
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                                                                                      /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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                                                   Consensus quality: 211691 bases at least Q40
Consensus quality: 216378 bases at least Q30
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Consensus quality: 216278 bases at least Q30
Estimated insert size: 218879; sum-of-contigs estimation
Batimated insert size: 218879; sum-of-contigs estimation
Quality coverage: 5.43 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a "working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                            ACLU9451 219679 bp DNA linear HTG 04-FEB-2002 HOMO Sapiens chromosome 5 clone RP11-170C8, WORKING DRAFT SEQUENCE, 9 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (04-FEB-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Homo sapiens (human)
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Center Code: JGI
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Gaps	CGAGITC CGAGIIC	CTTGTTT CCTGATG	GGTTGTA	GCTTGAT GCTGGAC	AAGGTAT CTGCTAT	CCTGTCT CACCACT	SATGACC CAACAGC	CATGCGT TAAGGAG	CTGGATC CTGGATC	CTGCATG CAGCATC	CTTTGAT GGTGGAT	GAAATGG	CAGTTGG	79	
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359;	CCATC AGTAC	TACCG CCGGG	ACTTA 	TTAGT - CAGC	TGGCC ATAGC	TCAAG CATC	CCATC CGGTC	AGCTA - AGTAC	GGACC 	TCAAC - TTCAT	GCTGI - GCATG	TCAAG	70090	GTGA1	
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Description	Abs54149 Human cDN	Acc50961 Human bla	Adn38833 Cancer/an	Aah48641 Human cer	Abs54148 Mouse cDN	Adi21948 Novel hum	Adl06640 Human 3T3	Adl06642 Human 3T3	Adi21468 Novel hum	Aak51566 Human pol	Aak52550 Human pol	Aah48639 Human cer	Abl24043 Drosophil	Abl30432 Drosophil	Abl24042 Drosophil	Adc87616 Human GPC	Ada71938 Rice gene	Ada71938 Rice gene	Abx74425 Human cDN	Abl90053 Human pol	Aah07955 Human cDN
SUMMARIES	ABS54149	ACC50961	ADN38833	AAH48641	ABS54148	ADI21948	ADL06640	ADL06642	ADI21468	AAK51566	AAK52550	AAH48639	ABL24043	ABL30432	ABL24042	ADC87616	ADA71938	ADA71938	ABX74425	ABL90053	AAH07955
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Score	828	813.6	813.6	761	664.8	486.2	414.8	414.8	313	185	185	183.4	147.8	92.6	75	52.2	44.8	41.2	40.2	40.2	40.2
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Aah48640 Human cer	Abz11993 Human pol	Adm44511 Novel hum	Aah15072 Human cDN	Aaa96499 cDNA enco	Abv27900 Human pro	Abv28037 Human pro	Abv22202 Human pro	Abv22064 Human pro	Abl24565 Drosophil	Abl24564 Drosophil	Ach93876 Human gen	Ach80176 Human gen	Aca57321 Human adi	Aah14050 Human cDN	Aba93743 Human tra	Abq60889 FLJ20756	Adc86916 Human GPC	Aas79600 DNA encod	Aaa10594 Gene enco	Aad07131 Canine re	Aad07132 Canine re	Aad07130 Canine re	2000 memin 37100 men
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40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.6	38.6	38	38	38	37.4
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ALIGNMENTS

RESULT 1

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Novel polypeptide designated as CRG-L1, useful as diagnostic marker for liver cancer, is differentially expressed in liver tumors relative to normal liver tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a polypeptide designated as CRG-L1), which is differentially expressed in liver tumours relative to normal expression
                                                                                                                                                                                          /*tag= a
/product= "Liver tumour marker protein, CRG-L1"
                                                                                Human cDNA encoding a liver tumour marker protein, CRG-L1.
                                                                                                     Human; 88; gene; liver cancer; liver tumour; CRG-L1; hepatocellular cancer; chromosome 9p.
                                                                                                                                                                Location/Qualifiers
1. .828
/*tag= a
          ABS54149 standard; cDNA; 828 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 8; 11pp; English.
                                                                                                                                                                                                                                                                         14-DEC-2001; 2001US-00017410.
                                                                                                                                                                                                                                                                                                  14-DEC-2000; 2000US-0255674P.
                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                            Farnham PJ, Graveel CR;
                                                                                                                                                                                                                                                                                                                        (FARN/) FARNHAM P J. (GRAV/) GRAVEEL C R.
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-706409/76.
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                                                                                                                                            Homo sapiens.
                                                        25-NOV-2002
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                                 ABS54149;
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RESULT

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               encoding polynucleotides (in the case of the human sequence, mapping to chromosome 9p), expression constructs, host cells, anti-CRG-L1 antibodies, identifying modulators of CRG-L1, and the use of the CRG-L1 sequence in the diagnosis of hepatocellular cancer in tumour cells from liver of a human or non-human animal. The CRG-L1 protein and polynucleotide are useful as diagnostic markers for a liver cancer in humans and non-human animals, and as a system for assessing putative therapeutic agents. The present sequence encodes human CRG-L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTATTTTCATTTTACCGCCCATCTGCATGTGCTTGTTTGATGAGTATGAGAACATGCTTG
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                                                                                                                                                                                      Sequence 828 BP; 157 A; 216 C; 211 G; 244 T; 0 U; 0 Other;
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                                                                                                                                                                                                                       100.0%; Score 828; DB 6; L 100.0%; Pred. No. 5.7e-242;
                                                                                                                                                                                                                                                             Mismatches
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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC5051 to ACC51059). ACC5051 to ACC51059 encode the human bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosting or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGACAACTACACCATCGTGCCTGCTATCGCCGAGTTCTACAACACGGTCAGCAATGTC 120
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patient with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting a bladder cancer-associated transcript in a cell patient, comprises contacting a biological sample from the
                                                                                                                 Human bladder cancer associated cDNA sequence SEQ ID NO:21.
                                                                                                                                                   Human; bladder cancer; cytostatic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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bladder cancer-associated polynucleotide or antibody.
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Pred. No. 3.4e-237;
0; Mismatches 9;
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              BP.
              ACC50961 standard; cDNA; 4202
                                                                                                                                                                                                                                                                                                                                                                                                                              EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                      03-JUL-2001; 2001US-0302814P.
03-AUG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-0350666P.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                        03-JUL-2002; 2002WO-US021338
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98.9%;
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Best Local Similarity 98.9°
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                                                                               (first
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                                              ACC50961;
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                   AACAGTGGCATCTACTTAATCTGGACTCTTTTGGTTGTAGTGGGAATTGGATCCGTCTAC
                                                                                                                                                                                                                                                                                                                                                                                               TCGGGCCTCTGGTGGACCCTGGTCTGTTCTGCTGGATCAGTGACCGAGCTTTCTGCGAG
AACAGTGACATCTACTTAATCTGGACTCTTTTGGTTGTAGTGGGAATTGGATCCGTCTAC
                                                          TICCATITIACCCTIAGITICITGGGTCAGAIGCTIGAIGAACTIGCAGICCTIIGGGTT
                                                                                                                       CTGATGTGTGCTTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAAGATCTTTCGGAAT
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                                                                                        TICCATGCAACCCTTAGITTCTIGGGICAGAIGCTIGAAGTTGCAGICCTTIGGGIT
                                                                                                                                                       CTGATGTGTGCTTTTGGCCATGTGGTTCCCCAGAGGTATCTACCAAAGATCTTTCGGAAT
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21-NOV-2001; 2001US-0332464P.
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention, antibodies which specifically bind a
polypeptide of the invention, use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
colypeptides and mucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
therosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistaion syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | TTCCAFTTTACCCTTAGTTTCTTGGGTCAGATGCTTGATGAACAACTTGCAGTCCTTTGGGTT 300
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Wilson KE, Zlotnik A;
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98.3%; Score 813.6; DB 11
Best Local Similarity 98.9%; Pred. No. 3.4e-237;
Matches 819; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID NO 151; 1385pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a nucleic acid in a biological sample.
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2001US-0334333P.
2001US-0340376P.
2001US-0340376P.
2002US-0347211P.
2002US-0347349P.
2002US-0355260P.
                                                                                                                                                                                                                                                                                                             (EOSB-) EOS BIOTECHNOLOGY INC
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                                                                                                                         2002US-0359077P.
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2002US-0396839P.
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Murray R,
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                                                                    10-JAN-2002;
08-FEB-2002;
13-FEB-2002;
                                                                                                                         20-FEB-2002;
29-MAR-2002;
04-APR-2002;
12-APR-2002;
29-NOV-2001;
03-DEC-2001;
14-DEC-2001;
08-JAN-2002;
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16-JUL-2002;
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Mack DH,
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This invention describes novel human ceramidase (I) containing a specific structural motif which has antiproliferative, anticancer, anti-eczema, antipsoriasis and dermatological activity. (I) cleave ceramide, resulting in formation of sphingosine. (I), or the nucleic acid (II) encoding it, are used for diagnosis, prevention or treatment of diseases associated with ceramide defects, particularly altered cell proliferation (cancer) or altered ceramide layers on the skin (neurodermatitis, eczema, psoriasis), also for targeted modification of the permeability barrier by ceramidase or its activators, e.g. for transcutaneous delivery of substances. Specifically they are used for diagnosis of ichthyosis, This sequence encodes human ceramidase K3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptide designated as CRG-L1, useful as diagnostic marker for liver cancer, is differentially expressed in liver tumors relative to normal liver tissues.
                      GCTGCCTACCTGGGCTGTGTATGCCTACTTTGATGCTGCCTCAGAGATTCCTGAG
                                                                                                             CAAGGCCCTGTCATCAAATTCTGGCCCCAGGGAAAATGGGCCTTCATTGGTGTCCCCTAT
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/product= "Liver tumour marker protein, CRG-L1"
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                                                                                                                                                                GTGTCCCTCCTGTGTGCCAACAAGAAATCATCAGTCAAGATCACG 825
                                                                                                                                                                                                             GIGICCCICCIGIGIGACAACAAGAAICAICAGICAAGACCACG 822
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse cDNA encoding a liver tumour marker protein, CRG-L1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; liver cancer; liver tumour; CRG-L1;
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35. .862
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                                                                                           1280 TGCTTTGCCTACTTTGATGCTGCCTCAGAGATTCCTGAGGCCAAGGTCTCATCATGAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang J;
Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTGTTTCGTCAAAGGTATCTACCAAAGATCTTTCGGAATGACCAGGGTAGGTTCAAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA,
Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT,
Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1623 BP; 305 A; 457 C; 382 G; 479 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                        19-SEP-2002; 2002WO-US029964.
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                                                                                                                 WO2003025148-A2.
                                                             Homo sapiens
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                       GATCTTTCGGAATGACAGGGGTAGGTTCAAGGTGGTGGTCAGTGTCTGCGGGTTAC
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              AGTCCTTTGGGTTCTGATGTGTGCTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAA
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                                                                                                     TCCTTGCACTGCACTGCTCATCGCAGAGCTAAAG-----
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                                                                                                                                                                                                                                                                                                                    Human 3T3 cell conversion promoter PP11646 DNA
                                                                                                                                                                                                                                                                                                                                   cell conversion; promoter; human; gene; ds
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/product= "PP11646"
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P-PSDB; ADL06641.
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This invention describes a novel human protein with 3T3 cell conversion promoting function, polynucleotides encoding the polypeptide and the recombinant process of producing the polypeptide. The present invention also discloses the agonist resisting the polypeptide and its treatment effect. The present invention also discloses the application of the polynucleotides encoding the human protein with 3T3 cell conversion promoting function.
                                                                                                                                                                                                                                                                                                                                                                                                                                           GATCAGCAATGTCTTATTTTCATTTTACCGCCCATCTGCATGTGCTTGTTTCGTCAGTA
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                                                                                                                                                                                                                                    Sequence 1527 BP; 376 A; 357 C; 383 G; 411 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                       17; Indels
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82.4%; Pred. No. 1.3e-115;
live 0; Mismatches 17;
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40 AGCTCGGAGGTGGACTGGTGCGAGGACAACTACACCATCGTGCCTGCTATCGCCGAGTTC
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                                                                                                             AAK51566 standard; cDNA; 1215
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27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-0059075.
19-JUL-2000; 2000US-00654936.
01-SEP-2000; 2000US-00654936.
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20-OCT-2000; 2000US-00693325.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C,
Ma Y, Zhao QA, 1
Xue AJ, Yang Y,
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                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                            AAK51566;
                                                                                                AAK51566
                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies, as markers for tissues in which the corresponding polypeptides, as markers for trissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in home cartiage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The
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                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
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ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue repair; tissue replacement; burn; incision; ulcer; cancer; human; ss; gene; EST; expressed sequence tag.
                                                                                                                                                                                                                                                                     Wang J;
Wang D;
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Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 719; 156pp; English.
                                                                                                                                                              19-SEP-2002; 2002WO-US029964
                                                                                                                                                                                         19-SEP-2001; 2001US-0323739P.
13-SEP-2002; 2002US-00323739
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                                                                                                                                                                                                                                                                                     Ghosh M, Xue AJ,
Haley-Vicente D;
                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
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                                                                                                WO2003025148-A2
                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                     Tang YT,
Ghosh M,
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The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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Chen R, Wang ZW;
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Vang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
459 CTGATGTGTGTTTAGCCATGTGGTTCCC 487
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AGCTCCGAGGTGGACTGGTGAGAGCAACTTCCAGTACTCGGAGCTGGTGGCCGAGTTC 139
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                                                                                                                                                                                                                                                                       Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 2079,
                                                   standard; cDNA; 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-FEB-2001; 2001WO-US004098
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                                                                                                            AAK52550
RESULT 11
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AAK52550

CTGGGAGTTCCTTGCACTGCACTGCTCATCGCAGAGCTAAAAGAGGTGTGACAACATGCGT

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and or activity activity and activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful in the diagnosis and to activity and may be useful and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the diagnosis and the di
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides with cytokine-like activities, useful
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Chen R, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1631 BP; 247 A; 399 C; 344 G; 350 T; 0 U; 291 Other;
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53.3%; Pred. No. 2e-45;
Live 0; Mismatches 360; Indels
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Mang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
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                       , 2000US-00496914.
; 2000US-00560875.
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                                                                                                                                                                                                                                                                                                                                                                Wang D, Wang
Wejhrman T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-476283/51.
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Ma Y, Zhao QA, Wa
Xue AJ, Yang Y, I
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P-PSDB; AAM79417.
                                                                                                        19-JUL-2000; 2
01-SEP-2000; 2
15-SEP-2000; 2
                                                    27-APR-2000;
20-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes novel human ceramidase (I) containing a specific structural motif which has antiproliferative, anticancer, anti-eczema, antipsoriasis and dermatological activity. (I) cleave ceramide, resulting in formation of sphingosine. (I), or the nucleic acid (II) encoding it, are used for diagnosis, prevention or treatment of diseases associated with ceramide defects, particularly altered cell proliferation (cancer) or altered ceramide layers on the skin (neurodermatitis, eczema, psoriasis), also for targeted modification of the permeability barrier by ceramidase or its activators, e.g. for transcutanceous delivery of substances. Specifically they are used for diagnosis of ichthyosis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ceramidase; human; K1; antiproliferative; anticancer; anti-eczema; antipsoriasis; dermatological; ceramide; sphingosine; treatment; ds; altered cell proliferation; cancer; neurodermatitis; eczema; cosmetic; permeability barrier; psoriasis; ichthyosis; lamellar ichthyosis ICR2.
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                                                                    GTGTTTAAGCTGGGCCTCTTCTCGGGCCTCTGGTGGACCCTGGCCCTGTTCTGCTGGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New ceramidase containing specific structural motif, useful for diagnosis, prevention and treatment of ceramidase defects, e.g.
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11-JUL-2000; 2000US-00614150.
                                                                                                                                  23-MAR-2001; 2001WO-US009231
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                                Drosophila melanogaster
pharmaceutical; gene;
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                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABR7072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCAACTTCCCCTACCTGC
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                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                             Drosophila melanogaster genomic polynucleotide SEQ ID NO 42769.
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ABL30432 standard; DNA; 4071 BP.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA acquences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences
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3404 ACTICTACGIGGAAICGGAGCIGCCCCAGCGACAGCCGCIGCIGAAGIACIGGCCAAAGA 3463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 GATCAGCAATGTCTTATTTTTACCGCCCATCTGCATGTGCTTTGATGAGTA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                 Drosophila melanogaster genomic polynucleotide SEQ ID NO 23599
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Best Local Similarity 55.6%; Pred. No. 1.4e-11;
Matches 144; Conservative 0; Mismatches 115; Indels
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11-JUL-2000; 2000US-00614150.
                                                                  3464 ACGAGTTCGAGTTC 3477
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288 AGTCCTTTGGGTTCTGATGTGTGCTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAA 347

228 TGGATCCGTCTACTTCCATTTTACCCTTAGTTTCTTGGGTCAGATGCTTGATGAACTTGC 287

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Db 3467 CATACTCGGGTCTTCATGGCGCCTTTTCGCTCTTCTATCCGAAGCGATACTATCCCAA 3526

Qy 348 GATCTTTCGGAATGACAGG 366

Db 3527 GTTCGTGAAAACGATCGG 3545

Search completed: November 20, 2004, 21:28:48

Job time : 355:193 secs
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Query Match
Best Local Similarity 99.1
Matches 109; Conservative
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CITY: Alexandria
STATE: VA
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ZIP: 22313-0299
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                                                                    November 20, 2004, 20:51:27 ; Search time 70.8343 Seconds (without alignments) 8308.591 Million cell updates/sec
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                                                                                                                                 atgggcgccccgcactggtg.......atcagtcaagatcacgtga 828
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/BCOMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-232-463-14
US-09-2007-005-17
US-09-244-796-17
US-09-184-796-17
US-09-189-039A-106
US-09-475-515-68
US-09-475-515-66
US-09-475-515-66
US-09-475-515-66
US-09-475-515-67
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US-08-480-751-1
US-08-943-986-1
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US-08-314-309A-3
US-08-164-839-30
                                                                                                                                                                                    824507 seqs, 355394441 residues
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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Fatent No. 6639063
GENERAL INFORMATION:
APPLICANT: Johnas Milne Edwards, J.B.
APPLICANT: Johnas Milne Edwards, J.B.
APPLICANT: Gloradano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFRENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
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US-08-164-839-32
US-08-583-799-30
US-08-583-799-32
US-08-164-839-69
US-08-164-839-71
US-08-183-71-18-1
US-08-314-309A-1
US-09-132-118-1
US-09-161-443-1
US-09-161-443-1
US-09-163-65-914
US-09-163-944-2
US-09-163-944-2
US-09-103-944-2
US-09-208-827-2
US-09-208-827-2
US-09-208-827-2
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-103-840A-2
US-09-103-840A-1
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; Patent No. 5670367
; GENERAL INFORMATION:
           4.1 2064 1 2064 1 2064 1 2064 1 2064 1 2064 1 2064 1 2064 1 2064 1 2064 1 2064 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066 1 2066
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APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
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LOCATION: (1)...(289)
   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                        SEQ ID NO 17
LENGTH: 289
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAK: (703)836-9300
                                                                                                                            FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 7218 base pai
TYPE: nucleic acid
STRANDEDNESS: single
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US-08-232-463-14
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RESULT 3 2-09-007-005-17/c ; Sequence 17, Application US/09007005B ; Patent No. 6258558

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507 TGACAACATGCGTGTGTTTAAGCTGGGCCTCTTCTCGGGCCTCTGGTGGACCCTGGCCCT 566
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Sequence 17, Application US/09244796

Fatent No. 6281344

JERERRAL INFORMATION:
APPLICANT: Scottak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: LOSCHEK, LABORITION: FURLENERENCE OF INVENTION: FURLENERENCE OF INVENTION: FURLENERENCE OF INVENTION: FURLONS;
TITLE OF INVENTION: FURLONS;
TITLE OF INVENTION: FURLONS;
CURRENT FILING DATE: 1999-02-05

CURRENT FILING DATE: 1999-02-05

EARLIER FILING DATE: 1997-01-27

EARLIER APPLICATION NUMBER: 60/064,491

EARLIER APPLICATION NUMBER: 60/064,491

EARLIER APPLICATION NUMBER: 09/007,005

EARLIER PILING DATE: 1999-01-06

EARLIER PILING DATE: 1998-01-14

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 289

"USBUST TO NOS: 200
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 0.7966/35.003
CURRENT APPLICATION NUMBER: 05/095/963
CURRENT FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
RARLIER PILICATION NUMBER: 60/055/491
EARLIER PLICATION NUMBER: 60/056/491
EARLIER PILICATION NUMBER: 60/056/491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.9%; Score 40.8; DB 3; Length 2 Best Local Similarity 6.9%; Pred. No. 0.011; Matches 15; Conservative 95; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                687 IGCCIACTITGAIGCIGCCICAGAGAITCCIGAGCA 722
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OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: RNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                    173 YNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYN 114
                                                                                                                                                                                                                                                                                                      627 CCTGCACTGCATGTGGCACATCCTCATCTGCCTTGCTGCCTACCTGGGCTGTGTATGCTT 686
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                                                                                                                     4.9%; Score 40.8; DB 3; Length 289; 6.9%; Pred. No. 0.011; tive 95; Mismatches 106; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: No. 6783969el Nucleic Acids and TITLE OF INVENTION: Polypeptides FILE REFERENCE: 803
                                                                                                                                                                                                                                                                                                                                                                  TGCCTACTTTGATGCTGCCTCAGAGATTCCTGAGCA 722
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: PL FL_genes Version 2.0
SEQ ID NO 875
LENGTH: 1063
FEATURE:
OTHER INFORMATION: Translation template
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 875, Application US/09799451
Patent No. 6783969
                                         ; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang, Jie
Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunqing
Yamazaki, Victoria
Chen, Rui-hong
Wang, Zhiwei
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Best Local Similarity 57.6%;
Matches 72; Conservative (
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Drmanac, Radoje T.
                                                                                                                   Query Match
Best Local Similarity 6.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
Ren, Feiyan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (2)..(802)
US-09-799-451-875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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Wang,
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APPLICANT:
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APPLICANT:
APPLICANT:
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7 GCCCCGCACTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGCGAGGAC

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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fink, Michel
APPLICANT: Basaye, Michel
APPLICANT: Basaye, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989.6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT APPLICATION NUMBER: 08/749,816
BARLIER FILING DATE: 1998-09-01
BARLIER FILING DATE: 1996-11-15
BARLIER FILING DATE: 1996-11-15
BARLIER FILING DATE: 1996-04-04
BARLIER FILING DATE: 1996-03-04
BARLIER FILING DATE: 1996-03-04
BARLIER FILING DATE: 1996-03-04
BARLIER FILING DATE: 1996-03-04
SOFTWARE: PATENTION NUMBER: FR 96/01565
NUMBER OF SEQ ID NOS: 24
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                                                                                          AACTACACCATCGTGCCTGCTATCGCCGAGTTCTACAACACGGATCAGCAATGTCTTATTT 126
                                                                                                                                                71 AACTACTCCGTGACCTGGTACATCGCCGAGTTCTGGAATACAGTGAGTAACCTGATCATG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           558
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559 CTGGCCCTGTTCTGCTGGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     499 AAGAGGTGTGACAACATGCGTGTGTTTAAGCTGGGCCTCTTCTCGGGCCTCTGGTGGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.5%; Score 37.4; DB 3;
50.9%; Pred. No. 0.41;
tive 0; Mismatches 86;
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; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09144914
Patent No. 6309855
GENERAL INFORMATION:
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Best Local Similarity 50.99
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Duprat, Fabrice APPLICANT: Lesage, Florian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: TASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (126)..(1307)
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                                                                                                                                                                                                                                                               131 ATTAT 135
                                                                                                                                                                                                         127 TTCAT 131
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US-09-489-039A-106
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                                    11
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US-09-475-515-65
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| Sequence 67, Application US/09475515A
| Patent No. 6602705
| GENERAL INFORMATION:
| APPLICANT: BARRET, Susan
| APPLICANT: SRIVASTAVA, Indresh
| APPLICANT: LIU, Hong
| APPLICANT: LIU, Hong
| APPLICANT: HARFOG, Karin
| APPLICANT: HARFOG, Karin
| APPLICANT: HARFOG, Karin
| APPLICANT: HARFOG, LALE
| APPLICANT: HARFOG, LALE
| APPLICANT: WALKER, Christopher
| APPLICANT: WALKER, Christopher
| APPLICANT: WALKER, Christopher
| APPLICANT: WALKER, Christopher
| APPLICANT: WALKER, Christopher
| TITLE OF INVENTION: INPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
| TITLE OF INVENTION: UNMBER: US/09/475,515A
| CURRENT PAPLICANTON UNMBER: US/09/475,515A
| UNMBER OF SEQ ID NOS: 90
| SOFTWARER PATENTIN VET. 2.0
| SROTTMARE PATENTIN VET. 2.0
| SROTTMARE PATENTIN VET. 2.0
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                                                                                                                                                                                                                                                                                                                                                                             486 CATCGCAGAGCTAAAGAGGTGTGACAACATGCGTGTGTTTTAAGCTGGGCCTCTTCTCGGG 545
                                                                                                                                                                                                                                                                                                                                                                                                                                      417 cericácicacecriacadadadadadadadadadadatadarecidarecadandanen 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              546 CCTCTGGTGGACCCTGGCCCTGTTCTGCTGGATCAGTGACCGAGCTTTCTGCGAGCTGCT 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    477 CAGCGCCTTCTTCGCGGCGCTGGTCAGCCTGATGCAGTACCTCGCCGACACGCGAAGAGAC 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537 Gradoceacarcerrandescrecadescreeceaceceaceceaces
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4.3%; Score 35.4; DB 4; Length 2340;
Best Local Similarity 57.8%; Pred. No. 1.6;
Matches 63; Conservative 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                      Query Match

4.3%; Score 35.8; DB 4; Length 1020;
Best Local Similarity 50.3%; Pred. No. 0.77;
Matches 88; Conservative 0; Mismatches 87; Indels 0
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OTHER INFORMATION: gp160.modUS4.delV1/V2
US-09-475-515-67
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 106
                                                                                                                                                 TYPE: DNA ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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SEQ ID NO 67
LENGTH: 2340
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                                                                                                                      LENGTH: 1020
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; Sequence 68, Application US/09475515A ; Patent No. 6602705

US-09-475-515-68

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APPLICANT: BARNETT, Susan
APPLICANT: STR MEGEDE, Jan
APPLICANT: STRVASTAVA, Indresh
APPLICANT: STRVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: Gratherine
APPLICANT: GEER, Catherine
APPLICANT: GEER, Catherine
APPLICANT: Mark
APPLICANT: Mark
APPLICANT: Mark
APPLICANT: Mark
APPLICANT: OF UNUBUTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES
FILE REPERBENCE: 1691-12-30
FURBERT PAPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 65
APPLICANT: ZUR MEGEDE, Jan.
APPLICANT: SURVASIAVA, Indresh
APPLICANT: SURVASIAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Hong
APPLICANT: LIU, Hong
APPLICANT: BLBY, Mark
APPLICANT: BLBY, Mark
APPLICANT: WALKER, Christopher
APPLICANT: WALKER, Christopher
APPLICANT: WALKER, Christopher
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: DY VIGS-LIKE PARTICLES
FILE REFERENCE: 1621.002
FILE REFERENCE: 1999-112-30
CURRENT FAPLICATION UNMERR: US/09/475,515A
CURRENT FILING DATE: 1999-112-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
LENGTH: 2385
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4.3%; Score 35.4; DB 4; Length 2385;
Best Local Similarity 57.8%; Pred. No. 1.6;
Matches 63; Conservative 0; Mismatches 46; Indels 0,
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4.3%; Score 35.4; DB 4; Length 2538;
Best Local Similarity 57.8%; Pred. No. 1.7;
Matches 63; Conservative 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: gp160.modUS4del 128-194
US-09-475-515-68
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; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: gp160.modUS4.delV1
US-09-475-515-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 65, Application US/09475515A; Patent No. 6602705
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ORGANISM: Artificial Sequence
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2427 GTÁCTIGGIGGAACCTIGCAGTACTIGGAGCCAGGAGCTIGAAGAGCAGCGCCGTGAGCT 2486
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                                                                                                                                                                                                                                                                                                                                                                                         12 GCACTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGCTGCGAGGACAACTA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 GCACTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGCGAGGACACTA 71
SEQ ID NO 64
LENGTH: 2634
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INPORMATION: Description of Artificial Sequence: gpl60.modUS4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 CACCATCGTGCCTATCGCCGAGTTCTACAACACGATCAGCAATGTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 CACCATCGTGCTGTTTCGCCGAGTTCTACAACACGATCAGCAATGTC 120
                                                                                                                                                                                                                                                             4.3%; Score 35.4; DB 4; Length 2634; 57.8%; Pred. No. 1.7; tive 0; Mismatches 46; Indels 0
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4.3%; Score 35.4; DB 4; Length 4472;
Best Local Similarity 57.8%; Pred. No. 2.4;
Matches 63; Conservative 0; Mismatches 46; Indels 0;
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OTHER INFORMATION: gp160.modUS4.delV1/V2.gag.modSF2
US-09-475-515-75
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; Sequence 73, Application US/09475515A
; Patent No. 6602705
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: SILVASTAVA, Indresh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 75, Application US/09475515A
Patent No. 6602705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                             Best Local Similarity 57.8
Matches 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-475-515-75
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                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BARNETY, Susan
APPLICANT: SUR MEGEDE, Jan
APPLICANT: SIVASITAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: GREER, Catherine
APPLICANT: SLEBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
ITILE OF INVENTION: OF VIRUS-LIKE PARTICLES
ITILE OF INVENTION: OF VIRUS-LIKE PARTICLES
ITILE OF INVENTION: OB9
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APPLICANT: BARNETT, Susan
APPLICANT: BARNETT, Susan
APPLICANT: STAVASTAVA, Indresh
APPLICANT: STAVASTAVA, Indresh
APPLICANT: LIAM, Ying
APPLICANT: LIAM, Ying
APPLICANT: LIAM, Warian
APPLICANT: HARTOG, Karian
APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: WalkER, Christopher
ITILE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REPERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT PILLING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
                                              2346 GTACTGGTGGAACCTGCTGCAGTACTGGAGCCAGGAGCTGAAGAGCAGCGCCGTGAGCCT 2405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71
   GCACTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGCGAGGACAACTA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 GCACTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGCGAGGACAACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: gp160.modUS4.delV2
                                                                                                                                                                                                                                                                                                                                                  Sequence 66, Application US/09475515A
Patent No. 6602705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
US-09-475-515-64
Sequence 64, Application US/09475515A
; Patent No. 6602705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICANT: HARTOG, Karin
APPLICANT: LIU, Hong
APPLICANT: Oatherine
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: MALKER, Christopher
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT PILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 GCACTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGCGAGGACAACTA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
4.3%; Score 35.4; DB 4; Length 4766;
Best Local Similarity 57.8%; Pred. No. 2.4;
Matches 63; Conservative 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: gp160.modUS4.gag.modSF2
US-09-475-515-73
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OPERATING SYSTEM: PC Comparible
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION 1435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: 08/353,784
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/22,827
FILING DATE: 23 August, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08485588
| Patent No. 5688938 | General No. 5688938 | General No. 5688938 | General No. 5688938 | General No. 5688938 | General APPLICANT: Steven C. Hebert APPLICANT: Steven C. Hebert APPLICANT: Orrest H. Fuller APPLICANT: James E. Garrett, Jr. TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE | TITLE OF INVENTION: MOLECULES | NUMBER OF SEQUENCES 20 | CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Lyon & Lyon STREET: First Interstate World Center STREET: Suite 4700 STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 633 West Fi
CITY: Los Angeles
STATE: California
COUNTRY: USA
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4.3%; Score 35.2; DB 1; Length 5
Best Local Similarity 50.6%; Pred. No. 3;
Matches 85; Conservative 0; Mismatches 83; Indels
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 PROPARTION:
ANNUEL US AND ASSETT TO A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT OF A REPORT 
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REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/005
TELECOMMUNICATION INFORMATION:
TELEFHOME: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR EQ ID NO: 1:
SEGUENCE CHARACTERISTICS:
LENGTH: 5275 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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nucleic acid
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LOCATION: 515..3769
OTHER INFORMATION:
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Search completed: November 21, 2004, 07:04:51 Job time : 75.8343 secs

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US-10-017-410-3
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17: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Appropriate 2 strains	Semience 21 Appl	Segmente 151 App	Semience 6 annie	Segmence 1, Appli	ς - • •	Segmence 40, Appl	Segrence 3, Appli	Semience 2069 An	Semience 77895		
ΩΙ	US-10-017-410-3	US-10-188-832-21	US-10-295-027-151	US-10-182-447-6	US-10-017-410-1	US-09-945-527-48	US-10-182-447-4	US-10-017-161-2429	US-10-292-798-2069	US-10-425-115-77895	US-10-437-963-77989	US-10-425-115-146588
DB	13	16	15	15	13	10	15	15	15	18	17	18
% Query Match Length DB	828	4202	4212	822	4175	744	792	35425	35425	3034	1604	637
% Query Match	100.0	98.3	98.3	91.9	80.3	42.3	22.1	6.3	6.3	5.1	5.0	5.0
Score	828	813.6	813.6	761	664.8	350.6	183.4	52.2	52.2	42.2	41.8	41
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Sequence 17, Appl	Sequence 615, App	2	87		322		equence			13	1369,	Sequence 24309, A	Sequence 86. Appl	Sequence 55, Appl	Sequence 3. Appli	Sequence 3, Appli	Sequence 7. Appli	Sequence 3722, Ap	Sequence 8306, Ap	Sequence 53388, A	Sequence 165, App	Sequence 311, App	Sequence 344, App	Sequence 344, App	344,	344,	344,	344	344,	a)	344,	e 344,
US-10-002-631C-1	US-10-264-237-	US-10-182-447-	US-10-	US-10-76	US-10-42	US-10-425	US-10-42	US-10-767-701-122	US-10-029-38	US-10-029	US-10-292-798-13	US-10-425-11	5-523-86	-60-	-484	-939-483	10-146-73	10-260-2	19-764-891-	-10-425-115-53	-10-388-934-	-10-191-803-31	-10-123-155-3	-10-146-731-	-10-140	-10	-10-14	-10	-10 - 13	-10-140-92	-10-141-75	US-10-141-759-344
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ALIGNMENTS

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Sequence 3, Application US/10017410
Publication No. US20020115094A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Farnham, Peggy J
APPLICANT: Graveel, Carrie R
TITLE OF INVENTION: Polymucleotide Differentially Expressed in Liver Cancer FILE REFERENCE: 960296.97401
CURRENT APPLICATION NUMBER: US/10/017,410
CURRENT FILING DATE: 2001-12-14
NUMBER: OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 828
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                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)..(825)
US-10-017-410-3
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SOFTWARE: Patentin Ver.
SEQ ID NO 21
LENGTH: 4202
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Publication No. US20040076955A1

GENERAL INFORMATION:

APPLICANT: Mack, David H.

APPLICANT: Aziz, Natasha

APPLICANT: Aziz, Natasha

TITLE OF INVENTION: Methods of Diagnosis of Bladder

TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

FILE REPRENCE: 018501-00230US

CURRENT FILING DATE: 2002-11-22

PRIOR APPLICATION NUMBER: US 60/302,814

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PRIOR FILING DATE: 2001-06-03

PRIOR FILING DATE: 2001-11-08

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                                                                        Length 4202;
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Pred. No. 2e-248;
0; Mismatches 9; Indels
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US-10-295-027-151
Sequence 151, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
                                                                        Query Match 98.3%;
Best Local Similarity 98.9%;
Matches 819; Conservative (
TYPE: DNA
ORGANISM: Homo sapiens
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506 480 900 989 099 720 806 998

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us-10-017-410-3.rnpb

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61 GAGGACAACTACACCATCGTGCCTGCTGGCCGAGTTCTATAACATGATCACGAATGTC 120
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                                                                                                                                                                               CTGCTCATCGCAGAGCTAAAGAGGTGTGACAACATGCGTGTGTTTAAGCTGGGGCCTCTTC
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                         GACCGGGGTAGGTTCAAGGTGGTCAGTGTCCTGTCTGCGGTTACGACGTGCCTGGCA
                                                                                           TCGGGCCTCTGGTGGACCCTGGCCCTGTTCTGCTGGATCAGTGACCGAGCTTTCTGCGAG
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                                                                  TITGICAAGCCTGCCAICAACAICTCTCTGTGACCCTGGGAGTTCCTTGCACTGCA
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96.0%; Pred. No. 5.4e-232;
ive 0; Mismatches 30;
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Matches 792; Conservative
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Best Local Similarity
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LENGTH: 822
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|TCCATGCAACCCTTAGTITCTTGGGTCAGATGCTTGATGACTTGCAGTCCTTTGGGTT 386
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APPLICANT: Matson, Susan R.
APPLICANT: Matson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Esca Biotechnology, Inc.
ITILE OF INVENTION: Methods of Diagnosis of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR PPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PLING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PLING DATE: 2001-11-29
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PRIOR PLING DATE: 2002-01-10
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PRIOR DATE: 2001-01-10-10-10-10-10-10-10-10-10-10-
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Afar, Daniel
Aziz, Natasha
Ginsberg, Wendy M.
Gish, Kurt C.
                                                                                 Glynne, Richard
Hevezi, Peter A.
Mack, David H.
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Best Local Similarity 98.9'
Matches 819; Conservative
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ORGANISM: Homo sapiens
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                               GAGGACAACTACACCATCGTGCCTGCTATCGCCGAGTTCTACAACACGATCAGCAATGTC 120
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Sequence 48, Application US/09945527

Publication No. US20030055588A1

SEGUENCE ACID MONETION:

TITLE OF INVENTION: No. US20030055588A1e1 Nucleic Acid Molecules Encoding TITLE OF INVENTION: No. US20030055588A1e1 Nucleic Acid Molecules Encoding TITLE OF INVENTION: Nucleic Acid and Protein Homologs

FILE REFREENCE: 35800/237985

CURRENT APPLICATION NUMBER: US/09/945,527

CURRENT FILING DATE: 2001-08-29

NUMBER OF SEQ ID NOS: 65

SOFTHARE: PASSEQ for Windows Version 4.0

LENGTH: 744
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35 ATGGGCCCCCCCCCCTGGTGGGACCACTGCGGGCTGCCAGTTCGGAGGTGGATTGGTGC
                                                 121 TTATITICATITIACCGCCCATCTGCATGTGCTTTGATGAGTATGCAACATGCTTG
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CORGANISM: Homo sapiens
US-09-945-527-48
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Publication No. US20020115094A1
GENERAL INFORMATION:
APPLICAMT: Farnham, Peggy J
APPLICAMT: Graveel, Carrie R
TITLE OF INVENTION: Polynucleotide Differentially Expressed in Liver Cancer
FILE REPRESENTE: 92096.974.07
CURRENT APPLICATION NUMBER: US/10/017,410
CURRENT FILING DATE: 2001-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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Pred. No. 6.5e-201;
0; Mismatches 102; Indels 0;
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ilarity 87.7%;
Conservative
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; LOCATION: (35)..(859)
US-10-017-410-1
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Best Local Similarity
Matches 726; Conserv
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UG-10-017-161-2429

Sequence 2429, Application US/10017161

Publication No. US20030143668A1

GENERAL INFORMATION

APPLICANT: SUMA, MAXIKO

APPLICANT: AAAL, KIYOSHI

APPLICANT: AAXIYAMA, YUTAKA

APPLICANT: ABURATANI, HIROYUKI

TITLE REFERENCE: 08435/0152

CURRENT FILING DATE: 2002-12-18

PRIOR APPLICATION NUMBER: UP 2001/246789

PRIOR PILING DATE: 2001-06-18

NUMBER: PATCH ONS: 2430

SOFTWARE: PATCHIN VOY: 2.1

SEQ ID NOS: 2430

LENGTH 1447
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FEATURE:
NAME/KEY: CDS
LOCATION: (21253)..(21367)
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ORGANISM: Homo sapiens
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NAME/KEY: source
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                    Score 350.6; DB 10; Length 744; Pred. No. 5.8e-101; 0; Mismatches 9; Indels 0:
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APPLICANT: HOFMANN, KAY
APPLICANT: HOFMANN, KAY
APPLICANT: RADT, MATCUS
TITLE OF INVENTION: CERAMIDASE
FILE REFERENCE: P68055USO
CURRENT FILING BATE: 2002-07-29
CURRENT FILING BATE: 2002-07-29
PRIOR PELICATION NUMBER: PCT/FP01/00900
PRIOR PLICATION NUMBER: DE 10003293.1
PRIOR PILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: DE 10011392.3
PRIOR APPLICATION NUMBER: B 10011392.3
PRIOR PILING DATE: 2000-01-27
PRIOR PILING DATE: 2000-01-27
SPIOR PILING DATE: 2000-01-27
SPIOR PILING DATE: 2000-01-27
SPIOR PILING DATE: 2000-01-69
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENT VET. 2.1
SEQ ID NO 4
LENGTH: 792
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Publication No. US20030185814A1
GENERAL INFORMATION:
                           42.3%;
                    Query Match
Best Local Similarity 97.5
Matches 356; Conservative
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; ORGANISM: Homo sapiens
US-10-182-447-4
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Sequence 77895, Application US/10425115
Sequence 77895, Application US/10425115
Publication No. US20040214272A1
Sequence 77895, Application No. US20040214272A1
SEQUENCE TO US CONTROL OF Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwal
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
CURRENT SILING DATE: 2003-04-28
SEQ ID NO 77895
LENGTH: 3034
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                                                                                                                                                                                                                                                                                                                                                                                                                          6.3%; Score 52.2; DB 15; Length 35425; 61.3%; Pred. No. 7.9e-05; tive 0; Mismatches 53; Indels 0;
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Pred. No. 0.036;
0; Mismatches 43;
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| NAME/KEY: CDS
| LOCATION: (35125)..(35225)
| FEATURE:
| NAME/KEY: modified base
| LOCATION: (35270)...(35369)
| COCATION: (35270)...(35369)
| COCATION: (35270)...(35369)
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. OTHER INTERPRETION: Clone ID: MRT4577_171063C.1
US-10-425-115-77895
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Best Local Similarity 61.3%;
Matches 68; Conservative (
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Best Local Similarity 61.3
Matches 84; Conservative
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(21462)..(21603)
                                                             (23918)..(24055)
                                                                                                          CDS (26460)..(26597)
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ORGANISM: Zea mays
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                                        NAME/KEY:
LOCATION:
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LOCATION:
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NAME/KEY:
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Fublication No. U5203033833A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ASAI, KIYOSHI
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT PILING DATE: 2002-11-13
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PATCHING UNCE: 2010-6-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PATCHING UNCE: 2.1
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Best Local Similarity 61.3%; Pred. No. 7.9e-05;
Matches 84; Conservative 0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: modified base
; LOCATION: (35270)...(35425)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-2429
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                                          (21462)..(21603)
                                                                                                          (23918)..(24055)
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(35125)..(35225)
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                                                             FEATURE:
NAME/KEY: CDS
LOCATION: (239)
FEATURE:
NAME/KEY: CDS
LOCATION: (264)
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US-10-292-798-2069
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LOCATION:
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FEATURE:
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LOCATION:
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FEATURE:
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                               527 AGCIGGGCCICITCICGGGCCICICIGGIGGACCCIGGCCCIGITCIGCIGGAICAGIGACC 586
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAI31P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
FRIOR APPLICATION NUMBER: PCT/US01/16450
FRIOR APPLICATION NUMBER: DG 60/205,515
FRIOR APPLICATION NUMBER: US 60/205,515
FRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PATENTIN VEY: 3.1
SEQ ID NO 615
LENGTH: 636
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Pred. No. 0.047;
0: Mismatches 53; Indels
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APPLICANT: Graff, Jonathon M.
APPLICANT: Muenster, Matthew
TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
FILE REFERENCE. A4943 090495.0243
CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 60/330,309
PRIOR FILING DATE: 2001-06-21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
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US-10-002-631C-17/c
US-10-002-631C-17/c
; Sequence 17, Application US/10002631C;
Publication No. US20030157486A1
; GENERAL INFORMATION:
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Publication No. US20040009491A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.9%;
Best Local Similarity 57.6%;
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CORGANISM: Homo sapiens
US-10-002-631C-17
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Li, Ping Tries Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE PREFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 77989
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APPLICANT: Kovalic, David K.
APPLICANT: Applicant Cao, Yongwei
TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 14658B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 CATGCGTGTGTTTAAGCTGGCCCTCTTCGGGCCTCTGGTGGACCCTGGCCCTGTTCTG 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               573 CTGGATCAGTGACCGAGCTTTCTGCGAGCTGCTGTCATCCTTCAACTTCCCCTACCTGCA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  633 CIGCAIGIGGCACAICCTCAICIGCCIIGCIGCCIACCIGGGCIGIGIAIGCI 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.0%; Score 41.8; DB 17; Length 1604; 52.6%; Pred. No. 0.035; tive 0; Mismatches 82; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.0%; Score 41; DB 18; Length 637; Best Local Similarity 52.7%; Pred. No. 0.039; Matches 89; Conservative 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_77836C.1
US-10-437-963-77989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: MRT4577_65204C.1
US-10-425-115-146588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(1604)
OTHER INFORMATION: unsure at all n locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 146588, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
                               Sequence 77989, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                       APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbaruk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.69
Matches 91, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays FEATURE:
                                                                                                           GENERAL INFORMATION:
US-10-437-963-77989/c
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NAME/KEY: unsure
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Job time : 389.775 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 AACTACACCATCGTGCCTGCTATCGCCGAGTTCTACAACACGATCAGCAATGTCTTATTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 AACTACTCCGTGACCTGGTACATCGCCGAGTTCTGGAATACAGTGAGTAACCTGATCATG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 AACTACACCATCGTGCTATCGCCGAGTTCTACAACACGATCAGCAATGTCTTATTT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 GCCCCGCACTGGTGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGCGAGGAC 66
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4.9%; Score 40.2; DB 16; Length 636;
Best Local Similarity 57.6%; Pred. No. 0.07;
Matches 72; Conservative 0; Mismatches 53; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.9%; Score 40.2; DB 15; Length 801;
Best Local Similarity 57.6%; Pred. No. 0.079;
Matches 72; Conservative 0; Mismatches 53; Indels 0.
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SQUENCE 5, Application US/10182447

Publication No. US20030185814A1

GENERAL INFORMATION:

APPLICANT: HOFMANN, KAY

APPLICANT: RADT, MARCUS

TITLE OF INVENTION: CERAMIDASE

TILE REFERENCE: P68055US

CURRENT APPLICATION NUMBER: US/10/182,447

CURRENT APPLICATION NUMBER: US/2001

PRIOR FILING DATE: 2002-07-29

PRIOR APPLICATION NUMBER: DE 10013293.1

PRIOR PILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: DE 1001392.3

PRIOR FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: DE 10011392.3

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 5

LENGTH: 801
                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
CCATION: (631)...(631)
COTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-615
NAME/KEY: misc feature
LOCATION: (560)..(560)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                              FEATURE:
NAME/KEY: misc feature
LOCATION: (605)..(605)
OTHER INFORMATION: n equals a,t,g, or
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; ORGANISM: Homo sapiens
US-10-182-447-5
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US-10-182-447-5
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Search completed: November 21, 2004, 07:44:02

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BX623644

UI-R-A0-a CCLX06a22

BF549345

CA967276 CA969385

BY117228 BY168309

CF593785 BE668106 220014 re BW216493

BX620332 BW215750 BW442024 AMGNINUC: M

BW215750

BW442024

BU337163 BX620332

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BW216493 AK075884

CB707581 CB298572

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                              AY401889 681 bp DNA linear GSS 12-DEC-2
Homo sapiens HCM1041 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 681)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGTGCTTGTTTCGTCAGTATGCAACATGCTTCAACAGTGGCATCTACTTAATCTGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 ATGTGCTTGTTTGATGAGTATGCAACATGCTTGAACAGTGACATCTAATCTGGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.1%; Score 671.4; DB 9;
99.1%; Pred. No. 2.7e-180;
ive 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 302 (5652), 1960-1963 (2003)
                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 681 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
CB723138
CB728612
CB706492
CF593785
BE68106
BY117228
BY168309
BY549345
CA967276
CA967276
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AL864302
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BW215750
BW442024
CB707581
CB298572
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                                                                                                                                                                                                  BW216493
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                                                                                                                                                                                                                                                                                                                   genomic survey sequence
                                                                                                                                                                                                                                                                                                                                        AY401889.1 GI:39757875
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                     Query Match 81.1
Best Local Similarity 99.1
Matches 675; Conservative
 sapiens
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 14671302
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210.2
198.6
194.4
191.8
188.2
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 300.2
299.8
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Gaps .; 0

Length 681; Indels

Result No.

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. FRATURES Location/Qualifiers Source /organism=Penn troglodytes" //mol type="genomic DNA" /db_xref="taxon:9598" /locus_tag="HCM1041"	Query Match 79.7%; Score 660.2; DB 9; Length 681; Best Local Similarity 98.1%; Pred. No. 4.2e-177; Matches 668; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	Qy 148 AIGIGCITGITIGAGAATAGCAACATGCTTGAACAGTGACATCTACTTAATCTGGACT 207	Qy 208 CITITGGINGRGAATIGGALCCGICIACITICCAITTACCCTIAGITICITGGGI 267 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	Qy 268 CAGATGCTTGATGAACTTGCAGTCCTTTGGGTTCTGATGTGTGCTTTGGCCATGTGGTTC 327	Qy 328 CCCAGAAGGTATCTACCAAAGATCTTTCGGAATGACAGGGGTAGGTTCAAGGTGGTGGTC 387 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 388 AGTGTCCTGTCTGCGGTTACGACGTGCCTGGCATTTGTCAAGCCTGCCATCAACATC 447	Oy 448 TCTCTGATGACCCTGGGAGTTCCTTGCACTGCTGCACTGCTGAGGGCTAAAGAGGTG 507	Qy 508 GACAACAIGCGIGIGITIAAGCTGGGCCTCTICTCGGGCCTCTGGTGGACCCTG 567	QY 568 TTCTGCTGGATCAGTGACCGAGCTTTCTGCAACCTGCTACACTTCCCCTAC 627 Db 421 TTCTGCTGGATCAGTGACCGAGCTTTCTGCGAGCTGTCTCTCTC
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Clark, A.G. Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriara, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
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/db_xref="taxon:10090"
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/tissue type="undiferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone lib="NHH MGC 134"
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI; Cloned undirectionally. Primer: Oligo dT. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NHH_MGC Library."
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                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                   Contract: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14067 row: j column: 05
High quality sequence stop: 681.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 5.1e-158;
0; Mismatches 114; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                 Mus musculus (house mouse)
Mus musculus
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Best Local Similarity 85.5%;
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AK085306 HTC 03-APR-2004 Mus musculus 0 day neonate Kidney CDNA, RIKSN full-length enriched library, clone:0630008P07 product:similar to CANCER RELATED GENE-LIVER 1 [Mus musculus], full insert sequence.
                                                                                                                              /tissue type="tumor, biopsy sample"
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/clone lib="NUC CGAP_Mam2"
/note="Organ: mammary, Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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                                                                  /db_xref="taxon:10090"
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/mol_type="mRNA"
/strain="FVB/N-3"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (baess 1 to 868)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://image.llh.gov
Plate: LLAM13955 row: g column: 14
High quality sequence stop: 679.
       CTCCTAGTTGTAGTGGGGATTGGATCTGTCTACTTCCATGCAACGCTGAGTTTCCTGGGT
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1173)
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                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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URL:http://fantome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                               Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTATTTTTCATTTTACCGCCCATCTGCATGTGCTTGTTTGATGAGTATGCACATGCTTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTTTTCATTTTACCTCCCCATCTGCATGTGCTTGTTCCGCCAGTACGCAACGTGCTTC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACAGGGGCAGGTTCAAGGCAGTGGTGTGTCTGTCTGCAATTACAACGTGCTTGGCG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGATGTGTGTTTTGGCCATGTGGGTTTTCCCAGGAGGTATTTACCAAAGATCTTTCGGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGGCGCCCCGCACTGGTGGGACCACCTGCGGGCTGGCAGTTCGGAGGTGGATTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGACAACTACACCATCGTGCCTGCTATCGCCGAGTTCTACAACACGATCAGCAATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCATTTTACCCTTAGTTTCTTGGGTCAGATGCTTGATGAACTTGCAGTCCTTTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCATGCAACGCTGAGTTTCCTGGGTCAGATGCTTGATGAACTTGCCATTCTGTGGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACAGGGGTAGGTTCAAGGTGGTCGTCAGTGTCCTGTCTGCGGTTACGACGTGCCTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGGCCTCTGGTGGACTCTGGCTCTTCTGCTGGATCAGCGACCAAGCCTTCTGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITGICAAGCCTGCCATCAACAACATCTCTCTGATGACCCTGGGAGTTCCTTGCACTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTATCAAGCCCGCCATCAACAATATTTCCCTGATGATTTCTGGGACTTCCATGCACTGCG
                                                                                                                                                                                                                              /note="unnamed protein product; putative
similar to CANCER RELATED GENE-LIVER 1 [Mus musculus]
(SPTR|AAL40408, evidence: FASTY, 100%ID, 77.8%length,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGGGCCCCCCCACTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGCTCATCGCAGAGCTAAAGAGGTGTGACAACATGCGTGTGTTTAAGCTGGGCCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  552 CTGCTTGTTGCAGAGCTGAAGAGGTGTGAATGTGCGTGTGTTTAAGCTGGGCCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1173;
                                                                                                                                               enriched mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCTGTCATCCTTCAACTTCCCCTACCTGCACGCATGTGG 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    672 CIGCICTCCCCTTCACTTCCCCTACCTGCACTGTGTGG 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 512.4; DB 3;
Pred. No. 8.4e-135;
0; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81;
/strain="C57BL/6J"
/db_xref="FANTOM DB:D630008P07"
/db_xref="taxon:10090"
/clone="D630008P07"
/tissue type="Kidney"
/clone lib="RIKEN full-length enr
/dev stage="0 day neonate"
                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/protein_id="BAC39416.1"
/db_xref="G1:26351559"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 61.9%; al Similarity 87.4%; 561; Conservative
                                                                                                                                                                                                                                                                                                                      match=642)
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RESULT

/organism="Mus musculus"

480 514 540 574 634

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Rattus.

1 (Dases 1 to 565)

Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V., Padua,A.M., Gurake,W.A., Morin,D., Penn,S.G., Jovanovich,S.B., Plopper,C.G. and Buckpitt,A.R.
Gene expression analygais in response to lung toxicants: I. Sequencing and microarray development
Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
Contact: Shultz MA
Contact: Shultz MA
Dept. of Molecular Biosciences, School of Veterinary Medicine
University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
Tel: 530 752 4698
Email: mashultz@ucdavis.edu
Average Phred score is 20 or better. All poor quality data (Phred < 20) and vector/linker sequence has been removed.
High quality sequence stope: 565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF115220 Shultzomica08471 Rat lung airway and parenchyma cDNA libraries Rattus norvegicus cDNA clone NP6159 S', mRNA sequence. CF115220. GI:33175919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue with the parenchyma" / tissue type="adult" / Clone lib="Rat lung airway and parenchyma cDNA libraries" / Clone lib="Rat lung airway and parenchyma cDNA libraries" / note="Organ: lung; Vector: pGEM-11Zf(-); Site_1: Eco RI; Site_2: Not I; mRNA was isolated from microdissected rat lung airways and parenchyma tissues."
                                                                                   395 GACAGGGCAGGTTCAAGGCAGTGGTGTGTGTCTGTCTGCAATTACAACGTGCTTGGCG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218 TAGTGGGAATTGGATCCGTCTACTTCCATT-TTACCCTTAGTTTCTTGGGTCAGATGCTT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                             GACAGGGGTAGGTTCAAGGTGGTGGTCAGTGTCCTGTCTGCGGGTTACGACGTGCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    readdecreragradacecertaricrecrearcagareagaeceaa-crirerecea
                                                                                                                                                                                             TITGLAAGCCIGCCAICAACAACAICICICIGAIGACCCIGGGAGIICCIIGCACIGCA
                                                                                                                                                                                                                                                             rrrarcaagcccgccarcaacaararrrcccrgargarcrcgggacrrccargcacrgcg
                                                                                                                                                                                                                                                                                                                                     CTGCTCATCGCAGAGCTAAAGAGGTGTGACAACATGCGTGTGTTTAAGCTGGGCCTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                            CTGCTTGTTGCAGAGCTGAAGAGGTGTGACAATGTGCGTGTGTTTAAGCTGGGCCTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGCTGT-CATCCTTCAACTTCCCCTACCTG 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      635 GCTGCTCCTTTTCACTTCCCCTACCTG 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="NP6159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.8
Matches 502; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
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                                         361
                                                                                                                                                                                                                                                                 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
CF115220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Jab host="DHIOR" (T1-phage-resistant)"
/lab host="DHIOR" (T1-phage-resistant)"
/clone lib="NIH MGC 169"
/clone lib="NIH MGC 169"
/note="Organ: Testicles; Vector: pDNR-LIB; Site_1: Sfil
(99ccattatgggc), Site_2: Sfil (99ccgcctggc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adapptors were used in cloning as follows:
5'-AAGGAGTGATACGAGAGTGGCATTACGGGGG3' and
5'-ATTCTAGAGGCGAGGCGACATG-dT (30)NN-3'. Full-length
enriched library was constructed using the Clontech
creator SMART kit and size-selected to contain the 0.5 kb
size fraction. Library created in thelaboratory of M.
Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
                                         EST 12-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TIATITITICATITITACCGCCCATCTGCATGTGCTTGTTTGATGAGTATGCAACATGCTTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 chdahdrigidchrinddccardrigidchriccadddahrinhaccaaagarchrinddaan 394
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 797)

NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                              CA463294 797 bp mRNA linear ES?
AGENCOURT_10691314 NIH_MGC_169 Mus musculus cDNA clone
IMAGE:6770649 5', mRNA sequence.
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/mol type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6770649"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                                                 CA463294.1 GI:24919646
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Matches 550; Conservative
                                                                                                                                                                                                                                                                                           Mus musculus
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J.,
Horno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Onno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
Unpublished (2001)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                              /clone lib="781 (synonym: hlcc4)"
/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2:
cDNA-collection"
                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                            Score 447.4; DB 5;
Pred. No. 2.3e-116;
0; Mismatches 1;
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/db_xref="taxon:9606"
/clone="DKFZp781B0790"
/dev_stage="adult"
/lab_host="DH108"
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BB660847.1 GI:16494626
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DKFZp781B0790_r1 781 (synonym: hlcc4) Homo sapiens cDNA clone
DKFZp781B0790_5', mRNA sequence.
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I (Dases 1 to 449)
Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wilmann, S.

EST (Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., et al.)
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This is the 5' sequence of the clone insert

Clone from 5. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKPZ); Email 8. Wiemann@dkfz- heidelberg.de;

sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing

consortium of the German Genome Project.

No sl sequence available.

This clone (DKFZP78180790) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGTGTGTTTAAAGCTGGGCCTCTTCTCTGGCCTTTGGTGGACTCTGGCTCTTCTGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 GAIGCIGCCICAGAGATACCCGAACAAGGICCAGICAICAGAITCIGGCCCAGIGAGAAA
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   TAGTGGGAATCGGGATCTGTCTACTTCCATNGCAACTCTTAGTTTCCTGGGTCAGATGCTT
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/mol_type="mRNA"
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TITLE JOURNAL COMMENT

AUTHORS REFERENCE

EST 26-0CT-2001

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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4396
Email: smithd@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmarch 12 options.
FOR PRIMERS
FOR PRIMERS
FORMARD: AGGAAACAGCTATGACCAT
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Bos taurus
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
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/lab_host="DH10B"
/clone_lib="MARC_2BOV"
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Seg primer: ATTTAGGTGACACTATAG.
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/db_xref="taxon:9913"
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transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5' Accordance of Sequence [5' Accordance of Sequence [5' Accordance of Sequence [5' Accordance of Sequence [5' Accordance of Sequence of Sequence [5' Accordance of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence of Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashiaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Yukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                               Email: genome-resegec.riken.jp, URL:http://genome.gec.riken.jp/
Carninci,P., Shibata,Y., Hayateu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayaehizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/tissue_type="kidney"
/dev_stage="0 day neonate"
/lab_host="DH10B"
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167

297 287 357 347 417 407 477

227

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698 bp mRNA linear EST 26-NOV-2002
CSEQCHN24 Gallus gallus cDNA clone ChEST757k21 5', mRNA
                                                                  /product="PP11646"
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ELAVLWYLMCALAMPRRYLPRYLPRNDRGRPKVVVSVLSAVTTCLAFVKPAINNISL
MTLGVPCTALLIAELKRHERNQRRRHRKGGQQGGGBKV"
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BU234223.1 GI:25478587
EST.
Gallus gallus (chicken)
Gallus gallus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                           GAICAGCAATGICITATITITICATITITACCGCCATCTGCATGIGCTTGTTTCGTCAGTA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             598 ACACAGGAAAGGIGGCCAGCAAGGAGGIGGAGACAAGGICIGACGAIGAGIGACICICIG
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                                                                                                                                                                                         Length 1527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                823
                                                                                                                                                                                        50.1%; Score 414.8; DB 3; Length 82.4%; Pred. No. 7e-107; ive 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                  GATCAGCAATGTCTTATTTTTCATTTTACCGCCCATCTGCATGTGCTT
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/organism="Homo sapiens"
            /mol_type="mRNA"
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                                                            /codon_start=1
                                         .640
                                                                                                                                                                                                                        Conservative
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Direct Submission
Submitsed (16-APR-2001) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/In 2200 Xie-Tu Road, Shanghai 200032, P. R. China
Location/Qualifiers
1. 1527
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Huang, Y., Zhou, X.M., Zhang, P.P., Jiang, H.Q., Qin, W.X., Zhao, X.T., Wan, D.F. and Gu, J.R.
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   /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
                                                                                                                                                                                                                                                                                                                                                                                            TCCATTTTACCCTTAGTTTCTTGGGTCAGAIGCTTGATGAACTTGCAGTCCTTTGGGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                          ACAGGGGTAGGTTCAAGGTGGTGTCAGTGTCTGCGGTTACGACGTGCCTGGCAT
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                                                                                                                                                                                                                                                                                                                                   182 ACAGIGACAICTACTIAAICTGGACTCTITTGGTTGTAGTGGGAATTGGAICCGTCIACT
                                                                                                                                                                                                                                                                                                                                                    TGATGTGTGCTTTGGCCATGTGGTTCCCCAGAAGGTATCTACCAAAGATCTTTCGGAATG
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                                                                                                                                                                                                                                                                        TATITITCATITITACCGCCCATCTGCATGTGTTTGATGAGTATGCAACATGCTTGA
                                                                                                                                                       TGGGCCCCCCCCTGGTGGGACCAGCTGCAGGCTGGTAGCTCGGAGGTGGACTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human cDNA clones with function of inhibiting cancer
                                                                                                                             1;
                                                                                               DB 4; Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                             Indels
                                                                                                                             43;
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Homo sapiens PP11646 mRNA, complete cds.
AF370405
                                                                                              50.3%; Score 416.2; DB '
llarity 91.1%; Pred. No. 2e-107;
Conservative 0; Mismatches 43
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Matches 453;
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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/cloud="Lines.1212.12"
//dev stage="122"
//lab_host="DH108"
//clone lib="CSEQCHN24"
//clone lib="CSEQCHN24"
//note="Organ: heads; Vector: pBluescript II KS(+); Site_l:
//note="Organ: heads; Vector: pBluescript II KS(+); Site_l:
//note="Constructed_from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
//was blunted, ligated to NotI adapters, digested with
// Rollowing this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
// EcoR. size-selected, and cloned into the NotI and EcoRI
// compatible sites of a custom modified MCS of the
// pBluescript (KS+) vector. The library was normalized in 2
// rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
// (1996): 791, except that a significantly longer
// reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BU232554 781 bp mRNA linear EST 26-NOV-2002
603409105F1 CSEQCHN24 Gallus gallus cDNA clone ChEST323j2 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Plassianinae; Gallus.

1. (bases 1 to 781).

Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                     361 AAAGCTITTIGIGAGAICTGGICAICATITAACTICCCCIAITTGCACTGIGIAIGGCAC 420
                                                                                                                                                                                                                                                                                   ATCCTCATCTGCCTTGCCTACCTGGGCTGTATGCTTTGCCTACTTTGATGCTGCC
                                                                                                                                                              706 TCAGAGATICCTGAGCAAGGCCCTGTCATCAAGTICTGGCCCAATGAGAAAIGGGCCTTC
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University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="White Leghorn, Hisex"
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1. .781
/organism="Gallus gallus"
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Tel: 01612008930
Fax: 01612360409
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/clone="ChEST323j2"
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/lab_host="DH10B"
/clonellab="CSEQCHN24"
/note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was intiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Pollowing this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
pBluescript (KG+) vector. The library was normalized in z
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
reannealing hybridization was used."
                                                                                     Bosch, E.,
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 698)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
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                                                                                                                                                                                                                                  Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
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Best Local Similarity 79.3%; Pred. No. 1.3e-103;
Matches 478; Conservative 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                             Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9031"
/clone="ChEST757k21"
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                                                                                                                                                                                                                 Contact: Simon Hubbard
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Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0812 row: G column: 07
Seg primer: M13 Reverse
High quality sequence stop: 548
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es 414; Conservative (
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Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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B0812G07-5 NIA Mouse Newborn Kidney CDNA Library (Long 1) Mus musculus CDNA clone NIA:B0812G07 IMAGE:30468654 5', mKNA sequence.
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
                                                                       Gaps
                                                                       5,
                   Length 781;
                                                                          Indels
                      Score 381; DB 5; Li
Pred. No. 2.6e-97;
0; Mismatches 125;
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// note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: Sall; Site 2: Not!; Mouse cDNA project by the Laboratory of Site 2: Not!; Mouse cDNA project by the Laboratory of GeneLics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgaun.grc.nia.nih.gov/CDNA). In brief, double-stranded cDNAs were synthesized with an Oligo (dT) primer [Invitrogen: S-pcAgraGTGGGGGGGGCGCCTTTTTTTTTTTT] from 5-pcAgraGTGTGGGGGGGGGCGCCTTTTTTTTTTTTTT] from 5-pcAgraGTGTGGTGGGGGGGGCGCCTTTTTTTTTTTTTT] in the contified by ethanol-precipitation. The CDNAs were ligated purified by ethanol-precipitation. The CDNAs were ligated separated from free linkers by Centricon 100. Then, the cDNAs were amplified by lorg-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Salf-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with Salf and Not! enzymes and cloned into Salf/Not! site of pCWV-SPORT6 plasmid vector. The DBINDB E. coll host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.0 kb. The library was constructed by Yulan Piao."
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/clone_lib="NIA Mouse Newborn Kidney cDNA Library (Long
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Pred. No. 5.8e-95;
0; Mismatches 69;
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421 AATATITCCCTGATGATTCTGGGACTTCCATGCACTGCGCTGCTTGTTGCAGAGCTGAAG 480

502 AGG 504 ||| 481 AGG 483

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Search completed: November 21, 2004, 06:57:34 Job time : 2289.57 secs